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Sequence for [1] kindly submitted on floppy by K.Kurachi, 05-AUG-1985.	AL		disequilibrium with two other F.IX polymorphisms Am. J. Hum. Genet. 42 (4), 573-580 (1988) 2450455 4 (Bites)	Wallmark, A., Ljung, R., Frazier, L.D., Ware, J.L., Lin, S.W., Stafford, D.W. and Bosco, J. The Malmo polymorphism of coagulation factor IX, an immunologic polymorphism due to dimorphism of residue 148 that is in linkage		5	Nucleotide sequence of the factor B) Biochemistry 24 (14), 3736- 2994716	<pre>Mammalia; Eutheria; Euarchontoglires; Primates; Cata Hominidae; Homo. E 1 (bases 1 to 38059) S Yoshitake,S., Schach,B.G., Foster,D.C., Davie,E.W. a</pre>	NISM	K02402.1 GI:182612 K02402.1 GI:182612 Alu repeat; Christmas facto; antihemophilic factor B; fac	'5 G HUMPIXG 38059 bp DNA linear PRI 30-APR-1996 TTION Human coagulation factor IX gene, complete cds.	1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705 	1621 GCCCAGTGGCTCACGCCTATAATCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680 	991 AATATATTTTTGTCTTCGCATATAAGTATAAAAAAAAAA	833			35653 CTTCTAGAGAGTIGCTGACCAACTGACGIAIGTITCCCTTTGIGAATTAATAAACTGGIG 35712 1381 TICIGGIICAIACCTIGGCIITIIGIGGAITCCAITGAIGIGAAICAGICACCCIGIAIT 1440

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FEATURES COMMENT REFERENCE TITLB JOURNAL AUTHORS mRNA gene SGO variation variation variation variation variation variation variation variation repeat\_region Bource repeat\_region repeat\_region Submitted (07-AUG-2002) Genome Sciences, University of Washington, 1705 NB Pacific, Seattle, WA 98195, USA To cite this work please use: SeattleSNPs. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu). Location/Qualifiers 1 (bases 1 to 35458) Rieder,M.J., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldanek,S.A., Rajkumar,N.R., Toth,B.J., Yi,Q. and Nickerson,D.A. Direct Submission /codon\_start=1 /product="coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)" /protein\_ida"AAM96188.1" /db\_xref="GI:22385321" /translation="MORVNMIMAESPELITICLLGYLLSAECTVFLDHENANKILNRP KRYNSGKLEEFVQGNLERECMEEKCSFEEAREVFENTERTREFWKQYVDGDQCESNPC LANGSCKDDINSYECMF9FGFEEGKNCELDYTCNIKNGRCEQFEKNSADNKVVCSCTEG YRLAENQKSCEBAVFFPCGRVSVSQTSKLTRAETVFPDVDYVNSTEAETILDNITQST QSFNDFTRVVGGEDAKGQFFMQVVLAGKVDAFCGGSIVNEKMIVTAAHCVEFGVKIT VVAGEHNIEETEHTEQKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPI CIADKEYTNIFLKFGSGYVSGWGRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYN NMFCAGFHEGGRDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRY VNWIKBKTKLT" /product="coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophila B)" join(1538. .1625,7859. .8022,8211 .8235,11929. .12042, j9217. \_19345,21916. .22118,31597. .31711,32380. .32927) /gene="F9" /frequency="0.02" /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" replace="t" gene="F9" replace="t" frequency="0.03" gene="F9" 147. 77. .1138 'frequency="0.05" replace="g" ĥ frequency="0.01" gene="F9" gene="F9" gene="F9" rpt\_family="L1" rpt\_type=dispersed replace="g" replace="c" replace="g" replace="c" frequency="0.50" frequency="0.15" rpt\_family="L1" rpt\_type=dispersed 23 vin(<1509..1625,7859..8022,8211..8235,11929..12042, )217.\_19345,21916..22118,31597..31711,32380..34316) requency="0.49" rpt\_type=dispersed 16 requency="0.47" .472 .35458 family="L1" .1229 .34316 variation variation repeat\_region repeat\_region repeat\_region repeat\_region variation variation variation variation variation cepeat\_region variation variation variation variation variation repeat\_region variation variation /replace="c" 5256 'gene="P9 frequency="0.01" ЪÇ. /replace="a" 2306 rpt\_family="MIR" gene="F9" -D D ĥ rpt\_family="MIR" replace=" g replace="a" frequency="0.12" frequency="0.04" replace="t" frequency="0.01" replace="a" replace="c" requency="0.42" |ene="F9" requency="0.01" jene="F9" yene="F9" replace="a" replace="t" gene="F9" gene="F9" frequency="0.01" frequency="0.49" gene="F9" rpt\_type=dispersed gene="F9" replace="a" frequency="0.02" gene="F9" "requency="0.01" ene="F9" requency="0.02" ceplace="a" replace="a" requency="0.03" replace="c" rene="F9" |ene="F9 "eplace="c requency="0.02" ene="F9" Ltype=dispersed \_type=dispersed \_family="MER2\_type" \_type=dispersed \_type=dispersed \_type=dispersed \_family="L2" ` \_family="L2" \_family="L2" .3596 .4469 .4261 .4410 5218 ٩ -

13216       TETECEANCEANAGESCULATION TO ATTACATACTACTACTACTACTACTACTACTACTACTACT	QY       1       ANTGANAGATUGATITICCANGGTIANTICATIGAAATUAACAGGCCTCTCAC       00         Db       32926       ANTGANAGATUGATITICCANGGTIANTICATIGGAATUGAAATUAACAGGCCTCTCAC       32985         QY       6.1       TPACTANTCACTITICCCANCETTUTUTTAGATUTUGAAATUAAAATUAACAGGCCTCTCAC       32985         QY       6.1       TPACTANTCACTITICCCATCTITUTUTAGATUGAAATUAAAATUAACATUCTATUGATCATUGCT       30.045         QY       1.21       TTTTCTCTTTACAGGGGAGAATUTCCATUTUTAAATUTUGAAATUAAATU	<pre>/replace="c" variation /gene="P9" /gene="P9" /frequency="0.48" /frequency="0.48" /frequency="0.48" /replace="a" variation 65316532 //replace="a" variation 6531.</pre>	<pre>repeat_region {replace="t" repeat_region 5842613 /rpt_family="Alu" /rpt_family="Alu" /rpt_requency="0.03" /frequency="0.03" /frequency="0.03" /replace="" /replace="" /frequency="0.05" /frequency="0.05" /freplace="" /replace="" /replace="" /replace=""</pre>	<pre>//gene="F9" //requency="0.49" /replace="t" /gene="F9" /gene="F9" /frequency="0.03" /replace="a" variation 5415 /frequency="0.47"</pre>	<pre>/frequency="0.02" /replace="g" S256 /gene="P9" /frequency="0.46" /replace="a" S265 /frequency="0.46" /frequency="0.46" /frequency="0.46" /frequency="0.46" /frequency="0.46"</pre>
	34006 1141 34066 1201 34126 1261 1261 1261 1321 1321 1321 1381 134306 1441	33826 961 33886 1021 33946 1081	721 33646 781 33706 841 33766 901	33466 601 33526 661 33586	33286 421 33346 33406 33406

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<pre>This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality &gt;= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. Location/Qualifiers source /organism="Nomo sapiens" /mol_type="genomic DNA" /db_xref="RXPD:RFOIP709D0788" /db_xref="taxon:9606" /map="q25-26.3"</pre>	<pre>OKGAMISM Homo Saptens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. REPERENCE 1 (bases 1 to 15857) ATTHORS Direct Submission JUTNAL Submitted (1:1-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Connerrequests: CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: CDINErequest@sanger.ac.uk Clone requests: CDINErequest@sanger.ac.uk clone requests: CDINErequest@sanger.ac.uk clone requests: Conserquest@sanger.ac.uk mumbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX WECTOR: pPAC4 </pre>	HUMARI Conta PTC, PTC, AL033 AL033 AL033 AL033 AL033	AGTGGCTCA.GGCTATAATCCCAGCACTTCTGGA.GGCCAAGGTGGGCGG 	1501 TGCCCCAACCTCACCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 1560 
mRNA .	gene	mRNA CDS	gene	gene mRNA
<pre>complement(5167961757), complement(5103561107) complement(5508959806), complement(5838558497) complement(5508955822)) /gene="MCF2" /locus_tag="R66-88D7.2-001" join(complement(AL161777.4:67777018), complement(125039125107), complement(120108105 complement(112887118977), complement(105654105 complement(114887118977), complement(105654105 complement(104714104330), complement(9951299626) complement(99942100075), complement(9951291023), complement(9950693025), complement(9832091023), complement(9920693025), complement(81020088071), complement(8162088577), complement(8101081098), complement(993279098), complement(7818878303), complement(793279098), complement(7818878303))</pre>	0024154" 740 Q95ND6 Q95ND r IX (plasma thre e, hemophilia B) LITICLLGYLLSARCT ELTICLLGYLLSARCT ESAREVPENTERTERT ENTRONECEOPED INTERNET ENTRONECEOPED INTERNET ENTRONECEOPED INTERNET ESTSFLTGIISWGEBEC EGTSFLTGIIS	<pre>/ Journa _ ray= ray= 0007.1-0029. J0475,14407. 14508,216822; join(407741)1,10329. J0475,14407. 14508,216822; /gene="F9" /locus_tag="RP6-88D7.1-002" /product="coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)" /note="match: HSTs: AV64051.1 AV698079. J0705,1439514 join(40844171,1032910492,1068110705,1439514 2168221810,2438124583,3406034174,348433539 /gene="F9"</pre>	/jocus_tag="Rp6.08D7.1.001" /product="coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B)" /note="match: ESTs: AI526776.1 AV647182.1 AV685937.1 AV687276.1 AV689501.1 AV69044.1 AV694632.1 AV695793.1 AV68721.1 AV696992.1 CB156396.1 CB157464.1 T28608.1 match: cDNAs: A13997.1 A22493.1 J00136.1 J00137.1 M11309.1 M21757.1 M23109.1 M26233.1 M26234.1 M26235.1 M26236.1 M26237.1 M26247.1 M33826.1 M35672.1 U51135.1 " Join(40774171,1032910475,1440714508,2168221711) /gene="pg"	/clone="RP6-88D7" /clone lib="RPCI-6" join(40774171,1032910492,1068110705,1439514508, 2168221810,2438124583,3406034174,3484336777) /gene=F9" /locus_tag="RP6-88D7.1-001" join(40774171,1032910492,1068110705,1439514508, 2168221810,2438124583,3406034174,3484336777) /gene=F9"

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mRNA	polyA_signal gene	mRNA	gene	mRNA	gene	polyA site
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QY       841       TATECCETEGTAGTAGACACACCACACACACATAATEGAAGCAATAAGCCATTCTA       900         Db       36227       TATECCETEGTEGTAGACACACCCCATACACACACATAATEGAAGCAATAAGCCATTCTA       900         QY       901       AGACCTTGTATEGTAGACACACACCCCATACACACACACAAGCAATAAGCCATTCTA       960         Db       36287       AGACCTTGTATEGTATAGGAAGCTCTGACCTAGGCATGACTACACACACACA	Db       36049       CATGTCTATCAACCCCAGACTUCCTUCCTADUCSADACTTCTTCAGAGAGTTAAGTTAACTATTTT         Qy       721       TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	541 CAAATCCCAATCCCCAATCAGTTTTTCTCTTTCTCTTTTTACCCTCCTTTTAACCCTCCTTTTTAACCCTCCT	421 : 35809 : 481 <i>J</i> 35869 <i>J</i>		181 ( 35569 ( 241 (	gene       complement(join(557625582,6103561107,6167961757,         Query Match       98.7%; Score 1684.6; DB 8; Length 158557;         Best Local Similarity       99.6%; Pred. No. 0;         Matches 1699; Conservative       0; Mismatches         Qy       1         AATGAAAGATGGATTICCAAGGITAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC         Gy       1         Db       35389         AATGAAAGATGGATTICCCAAGGITAATTCATTGGAATTGAAAATTCAATGGGCCTCTCAC         QY       61         TAACTAATCACTTTCCCAATCTTTTGTTAGATTTGAAATATAACATTCTATGGAATTGATAGATCATTGCT         QY       61         Db       35449         DAATTCAAATCACTTTCCCAATCTTTTGTTAGATTTGAATATATAACATTCTATGATCATTGCT         QY       121         TTTTCTCTTTACAGGGGAGAATTTCAATTTCATATTTAACATTCTATGAAAATGGAA         Db       35409         DA       35509         TTTTCTCTTTACAGGGGAGAATTTCATATTTAACTGCTGAGCAAATTGATTAGAAAATGGAA         Db       35509         TTTTCTCTTTACAGGGGAGGAATTTCATATTTAACTGTGAGCAAATTGATAGATA

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<pre>RESULT 8 HUMFIXG6 LOCUS BEFINITION ACCESSION VERSION K02053 1 GI:182619 VERSION K02053 1 GI:182619 SEGMENT G of 6 SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (human) Nutrions Sapiens (human) AUTHORS AUTHORS 1 (bases 1 to 3121) AUTHORS Anson, D.S., Choo, K.H., Rees, D.J., Giannelli, F., Gould, K., Huddleston, J.A. and Brownlee, G.G. AUTHORS 2 (bases 3011 to 3012; 3026 to 3028; 3090 to 3092) AUTHORS Anson, J.A. and Brownlee, G.G. JOURNAL PUBMED 2 (bases 3011 to 3012; 3026 to 3028; 3090 to 3092) AUTHORS Anson, J.A. and Brownlee, G.G. UNINAL PUBMED 2. (bases 3011 to 3012; 3026 to 3028; 3090 to 3092) Huddleston, J.A. and Brownlee, G.G. JOURNAL PUBMED 2. (bases 3011 to 3012; 3026 to 3028; 3090 to 3092) Huddleston, J.A. and Brownlee, G.G. Unpublished (1985)</pre>	Db       36647       TITCIGGTTICGTGTCACCATGGAACATTIGATTATAGTTATCCTTCATGATCATCATCAACTGGTG         QY       1321       CTTCTAGAGAGTTGCTCACCAACTGACGTATGTTTCCCTTTGTGAATTAAACTGGTG       130         Db       36707       CTTCTAGAGAGTTGCTGCCCAACTGACGTATGTTTCCCTTTGTGAATTAAACTGGTG       1676         QY       1381       TTCTGGTTCAAGAGTTGCTGGCCTTGTTGGAATTCAATTAATAACTGGTG       1676         QY       1381       TTCTGGTTCAAGAGTTGCTGGCCTTGTTGGAATTCAATTCAACTGGTGAACCATTGTTGTGAATTAAACTGGTG       1676         QY       1441       TGATGATGCATGGAACATTGTGGAAAAATCACTCTGGAACGTGGTGCTGCCTTCTCC       3686         QY       1441       TGATGATGCATGGAACTACTGAACAAAATCACTCTGGAAGCTGCTGCCTTCTCC       3686         9b       36827       TGATGATGCATGGAACTACTGAACCAACTCACTCCTGGAAGCTGCTGCCTTCTCC       3686         9c       1501       TGCCCCAACCTAACCCCAAGCCAAGCCTCACTCCTGCAATTAATT	1021       TAATAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTT
old_sequence       3090.302         ORIGIN       About 9.96 kb after segment 5; chromosome Xq26.3-q27.2.         Query Match       95.2%; Score 1624.8; DB 8; Length 3121;         Best Local Similarity       95.3%; Pred. No. 0;         Matches 1642; Conservative       0; Mismatches       2; Indels         Qy       1       AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAAATGAAATTAACAGGGCCTCTCAC       60         Db       1472       AATGAAAGATGGATTTCCCAAGGTTAATTCATTGGAAATGAAAATTAACAGGGCCTCTCAC       1531         QY       61       TAACTAATCACTTTCCCAAGGTTAATTCATTGGAAATGAAAATTAACAGGGCCTCTCAC       1531         Db       1472       AATGAAAGATGGATTTCCAAGGTTAATTCATTGAATATAACAGGGCCTCTCAC       1531         QY       61       TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATAACATTGAATACAGGGCCTCTCAC       1591         Db       1532       TAACTAATCACTTTACGAGGAGAAATTGAATTGAAATTGAAATGGAAAATGGAA       180         Db       1592       TTTCTCTTTACAGGGGAGAAATTTAAGGGAAAATTGAAATGGAAAATGGAA       1651         QY       181       CCACTAGAGGAATATATATGTGTTAGGAATTCAATTACAGTCAATTGAAATGGAAAATGGAA       1651         Db       1592       CCACTAGAGGAATATATAATGTGTTAAGGAAATTAAGGTCAATTCAATTGAATAGGCCCAGCCCTTGA       240         Db       1652       CCACTAGAGGAATATAATATATAGTGTTAAGAATTAAAGTCATTCTAAGCCAGCC	<pre>//b.vref="01:19821" /translation="WORVNHMASSPGLITICLLGYLLGARGEVPENDENANNTLINE KIXYNGGLEERVOGULEEROWERKGSPENARVPENTERVTERVECODOCESNNC LNGGSCKDDINSYEGWEPFGFEEGKNCELDVTCNIKNGRCEOFCKNSADNKVVCSCTEG YELAENQCSCEBAVFFGFEKKVSGGSLAVTCNIKNGRCEOFCKNSADNKVVCSCTEG YELAENQCSCEBAVFFGFEKKVSGGSLAVTCNIKNGRCEOFCKNSADNKVVCSCTEG YELAENQCSCEBAVFFGFEKKVSGGSLAVTRALALELDEFLVLNSYTFJ CYNACEHNEGSCAVGGENWGVVLNGKVARGCGSIVUKSTEALTILNNITGST VNACEHNEGGSUSGGENVVLRIIPHNYNAAINKYNHDIALLELDEFLVLNSYTFJ CYNACEHNEGGSUSGGENVVLRUGSGAUVUKURSTEALTILNNITGST VNACEHNEGGSUSGGENVVLRUGSGAUVUKURSTEALTILNNITGST VNACEHNEGGSUSGGENVVLRUGSGAUVUKURSTEALTILNNITGST VNACEHNEGGSUSGGENVVLRUGSGAUVUKURSTEALTILNNITGST VNACEHNEGGSUSGGENVVLRUGSGAUVUKURSTEALTILSDEFLVLNSYTFJ CYNACEHNEGGSUSGGENVVLRUGSGAUVUKURSTEALTILSDEFLVLNSYTFJ (20251.1:1.360,K02052.1:1.599,K02050.1:1.240, /note="fixili:.360,K02052.1:1.360,1.257) /note="fixili:.360,K02052.1:1.360,1.257) /note="fixili:.360,K02052.1:1.360,1.257) /note="fixili:.360,K02052.1:1.360,1.257) /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.360,K02052.1:1.360,1.257] /note="fixili:.3012 /number=0 /number=1 /number=6 /number=5 /number=5 /number=5 /number=6 /number=6 /number=6 /number=6 /number=6 /number=6 /number=7 /number=6 /number=6 /number=6 /number=7 /numb</pre>	<pre>COMMENT Original source text: Human: cDNA to liver mRNA, clones cVII, cVI, 108.1, and DB.1; 4X lymphoblastoid cell line (GM1416B) DNA, clone lambda-HIX-1, 2, 3. [2] reviees [1]. See segment 1. See segment 1. I3121 /organism="Homo sapiens" /map="x26:3-q27:1" db_xref="senonic DNA" /map="x26:3-q27:1" join(K02049.1:325.412,K02049.1:176339, K02049.1:528.[552,K02050.1:65179,K02051.1:143271, K02052.1:82384,143257,9261473) /note="factor IX" /codon_start=1]</pre>

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1201       111111111111111111111111111111111111		AGTTGCCTAGACCAGAGGACATAAGTAATCATGTCTCCTTTAACTTAACCATACCCCGAAGTG 	1081       CTTTEAGGAAGATTCAACAGTGTGTGTCTCAGGAGTGTCAGAGCCAAGCAAG	1080	961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020 	901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGACTTTCACGAAGGCAAGATTGGCAT         960         Que           1	841         TATGCGTGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA         900         \$           1	781       ATATATATAATATATATATATATATATATATATATATA	721       TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	661       CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA       720       ACCESSION         1	601       CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA       660       RESULT       9         801	541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTACTCCCTCTCTCCCCTTTTACCCTC 600 	481 AAACTCATCAAAAAACACTACTCCTTTTCCCTCTACCCTATCCTCAATCTTTTACCTTTTC 540       0         1	421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACAAGAACAGGAGTAGCTGAGAGGCTA 480 	361       TCTCCAACCAAAACATCAATGTTTAATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC       420       Db         1832       TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC       1891       Db	301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360 Db 	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCACTATGGTTCTCCACTATGG 1771 Db 
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Qy 1381 TTCTGGTTCAT 1391 Db 2765 TTCTGGTTCAT 2775	1 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1 	Oy         1261         TELEFORGETTECACCATEGAACATETTGATTATAGETAATACTECTATCETGAAT         1320           Db         2645         TELEFORGETTCCACCATEGAACATETTGATTATAGETAATCCTTCTATCETGAAT         2704	Qy         1201         Gagaagggggcagcagcagggcagggcagggcagggggggg	Qy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG       1200         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy       1081       CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	Oy         1021         таатаатаатастаасладаадаадаадаадаассертгерстарсаартсасларстараадаа         1080           U	Qy         961         ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA         1020	Qy 901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960 	841 TATGCGTGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 9 	Qy         781         ататататататататататататататататататат	Oy         721         TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	Qy         661         CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA         720	Qy       601       CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA       660	Oy         541         CANATECECANTECECANATEAGETETETETACTECETETECETACECECTETTACECET         600           []]][]][]][]][]][]][]][]][]][]][]][]][]	481       AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC         1   .		361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 
<pre>variation /gene="F9" /note="g in wt; a in hemophilia Seattle 3 (Glu-&gt;Lys) [2]" variation 316 /gene="F9" /note="g in wt; a in hemophilia Durham (Gly-&gt;Ser) [2]"</pre>	peptide 6	factor IX light chair	<pre>sig_peptide /gene="P9" /gene="P9" /note="coagulation factor IX signal peptide" mat_peptide 139573</pre>	t	LNGSSCKDINS VEGEDARDE DUTCHIKKGRCEGPEKKSADKKVCSCTEG TYRLAENQKSCEPAVPFPCGRVSVSQTSKLTRAETVFPDVDVVNSTEAETILDNITQST QSFNDFTRVVGGEDARDGPPQVVLNGKVDAFCGGSIVNBKUTALLEDDALCVETGVKIT	/db_xref="GI:180553" /db_xref="GDB:GO0-119-900" /translation="GDB:GO0-119-900" /rranslation="GDB:GO0-119-200"	/gene="F9 /note="cc /codon_st	mRNA /gene=P99 /product="CIX mRNA" CDS 11386		e Location/Qualifiers .e /organism="Homo sapiens" /mol type="mRNA"	in their hemophilic proteins Invest. 84 (1), 113-118 (1989) Source text: Human liver CDNA to mRNA.	REFERENCE 2 (bases 214 to 222; 313 to 321; 877 to 885) AUTHORS Chen,S.H., Thompson,A.R., Zhang,M. and Scott,C.R. TITLE Three point mutations in the factor IX genes of five hemophilia B patients. Identification strategy using localization by altered	TITLE Bridence for a prevalent dimorphism in the activation peptide of human coagulation factor IX JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82 (9), 2847-2851 (1985)	Hominidae; Homo. REFERENCE 1 (bases 1 to 2775) AUTHORS McGraw,R.A., Davis,L.M., Noyes,C.M., Lundblad,R.L., Roberts,H.R., Graham J R and Stafford D W	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;	VERSION M1109.1 GI:180552 KEYWORDS clotting factor; clotting factor IX; coagulation factor; coagulation factor IX; factor IX.	RESULT 10 HUMCIX LOCUS HUMCIX 2775 bp mRNA linear PRI 01-NOV-1994 DEFINITION Human coagulation factor IX mRNA, complete cds.

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Matches 1391; Conservati 1 ANTGANAGARGA 61 FRACTANCACTT 1445 FRACTANCACTT 121 TTTTCTCTTTACA 1505 TTTTCTCTTTACA 1505 TTTTCTCTTTACA 15165 CCACTAGAGGAAT 1565 CCACTAGAGGAAT 1565 CCACTAGAGGAAT 1625 CCACTAAGTGAGGAAT 1625 CCACTAAGTGAGGAAT 1625 CCACTAAGTGAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1625 CCACTAAGTGAAGGAAT 1631 TCTCCCAACTAACTCACT 421 TCTATCACAAGGGC 481 AAACTCCATCACTAAGGGC 601 CATGGTCGTTAAAATCCCAATCC 601 CATGGTCGTTAAAGGTGC 721 TGAAGTAAGTCACTAAGGTGC 721 TGAAGTAAGGTGC 731 ATATATATATATATATAT 841 TATGCGTGTGTGTGT 901 AGAGCTTGTATGG	variation 56 // variation // variation // N Chromosome ry Match // t Local Similarity
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421 421 1805 1865 541 1925 601 1985	241 CAAAATTGTGAAGTTAAATTGTCCACTCGTGTGCCATCAGATACTATGGTTCTCCACTATGG 241 CAAAATTGTGAAGTTAAATTGTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 1625 CAAAATTGTGAAGTTAAATTCTCCCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 301 CAACTAACTCACTCAATTTTCCCCTCCTTAGCAGCAGTCCATCTTCGGTTCTCTTTGCT 1685 CAACTAACTCACTCAATTTTCCCCTCCTTAGCAGCAGTTCCATCTTCCCGATCTTTCGTCTTGCT 361 TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTCGTTCTAG 361 TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTCGTTCAC 361 TCTCCCAACCAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTCGTTCTAC	Qy       61 TAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120         Db       1445 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504         Qy       121 TTTTCTCTTTACACGGGAGAATTTCATATATTGAATATACATTCTATGAATATGGAT 180         Db       1505 TTTTCTCTTTACAGGGGAGAATTTCATATATTTACCTGAGCAAATTGATTAGAAATGGAA 1564         Qy       181 CCACTAGAGGGAGAATATTAGTGTTAGGAATTTCATATTACATTCTAAGGCCAACCCCTTCA 240         Qy       181 CCACTAGAGGGAATATAATGTGTTAGGAAATTTCATATTTACGTCATTTAGGAATTGAATAGGAA 1564         Db       1565 CCACTAGAGGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGCCCAACCCCTTCA 1674	1arity 81.5%; Score 1arity 100.0%; Pred Conservative 0; Mi GAAAGATGGATTTCCAAGGTTA                    GAAAGATGGATTTCCAAGGTTA	<pre>Prepared with primer pairs provided by Sandoz, derived from M11309 Washington University/Merck EST sequence. PEATURES Location/Qualifiers source 12775 /organism="Homo sapiens" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="texton:9606" /map="X" STS 21092327 primer bind complement(23052327)</pre>	Primer: each 1 um dwrPe: each 200 um Tag Polymerase: 0.05 units/ul Total Vol: 10 ul . Buffer: MgCl2: 2.5 mM KCl: 50 mM pH: 8.3
LUCUS DEFINITION DEFINITION Sequence 40 from Patent W02004083404. ACCESSION VERSION CQ882048.1 GI:54034760 KEYPORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM Homo sapiens ORGANISM Homo sapiens UNATYORA; Retazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Eutechontoglires; Primates; Catarrhini; Hominidae; Homo. 1 AUTHORS 0i,Y., Zhang,X. and Konigsberg,P.J. JOURNAL Patent: W0 2004083404-A 40 30-SEP-2004; Isogenis, Tanc. (US) FEATURES Source /organism="Homo sapiens" /mol_type="unassigned DNA"	GAGAGTTGGTGACGTAACTGACGTATGTTTCCCTTTGTGAATTAATAAA 	0y       12525       AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCAGAGTG 2564         0y       1201       GAGAAGGGTGCAACAGGGCTCAAAGGCATAAGTATCATGTCCCTTTAACTAGCATACCAGCAAAGTG 2564         0y       1201       GAGAAGGGTGCAACAGGCTCAAAGGCATAAGTCATCCCAATCAGCCAAACTAGTTGTCCT 1260         0b       2585       GAGAAGGGTGCAACAGGCTCAAAGGCATAAGTCATCCAATCAGCCAAACTAAGTTGTCCT 2644         0y       1261       TTTCTGGTTTCGTGTTCACCATGGAACATTTTGAATTATAGTTAATCCGTCTTCTAACTTGAAT       1220         0y       1261       TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTAACTTGAAT       1320         0b       2645       TTTCTGGTTTCGTGTTCACCATGGAACATTTGATTTATAGTTAATCCTTCTAACTTGAAT       1320	1021       TAATAATAGTGATAATAGCAGAAGAAGAAGAAGAAGAACCGTTCGTT	Qy       841       TATGCGTGTGTGTGTAGACACACACACACACACACACACA	Db       2045       CANGTERTATIONAGE CENSAGETISCETICCATAGETISCETICAGAGAGETISCETITECAGAGAGETATETT       780         QY       721       TGAAGETAAGGETIGCETIGGETIGGETIGGETIGGAGAGAGETISCETITECAGAGAGETAAGETATETT       780         Db       2105       TGAAGETAAGGETIGGETIGGETIGGGAGAAAGETISCETITECAGAGAGETAAGETATETT       780         Db       2105       TGAAGETAAGGETIGGETIGAAAAGETISCETISCEGAGAAAGETISCETISCAGAGAGETAAGETIATETIS       2164         QY       781       ATAATATATAATATATATATATATATATATATATATAT

$ \begin{array}{c} \textbf{Oy} & \textbf{181}  CCACTAGAGGAATATAATGTGTTATAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA \ 240 \\                                     $	961	_
$\begin{array}{llllllllllllllllllllllllllllllllllll$	Oy         901         Agagetterategatategateterategateterategateterategaagecaagattegeat         960           []]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]	
OY 61 TAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120 	Oy         841         TATGCGTGTGTGTGTGACACACACACGCATACACACATATAATGCAAGCAA	
	$\begin{array}{llllllllllllllllllllllllllllllllllll$	
	Oy         721         TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	
/organism="unknown" /mol_type≃"genomic DNA"	Oy         661         CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA         720	
JOURNAL Patent: US 6677369-A 2 13-JAN-2004; Eli Lilly and Company; Indianapolis, IN FEATURES Location/Qualifiers source 1. 2804	Qy         601         CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA         660         111111111111111111111111111111111111	
	Oy         541         CAAATCCCCAATCCCCAAATCAGTTTTCTCTTTCTTACTCCCTCTCCCTCTTACCCCCC         600           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
<ul> <li>M Unknown.</li> <li>Unclassified.</li> <li>1 (bases 1 to 2804)</li> <li>3 Beight, D.W., Craft, T.J., Franciskovich, J.B., Goodson, T. Jr.,</li> </ul>	OY         481         Amactcatcananancactactcetttecetetaccetattecetareettetacettette         540           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
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RESULT 13 AR452580 LOCUS AR452580 2804 bp DNA linear PAT 20-FEB-2004 DEFINITION Sequence 2 from patent US 6677369.		
2794	Oy         301         CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCCGATCTTCTTTGCT         360           111111111111111111111111111111111111	•
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Db 2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCGAGACATATTGTACTCTTTCTAAAAAAIAA 2433 Qy 1021 TAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080	/db_xref="taxon:9606" ORIGIN	-

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OY 1261 TETCEGETECETE 	QY 1201 GAGAAGGGTGCAGC                  Db 2614 GAGAAGGTGCAGC	Qy         1141         AGTTGCCTAGACCA   Db         2554         AGTTGCCTAGACCA	Oy 1081 CTTTGAGGAAGAAT                    Db 2494 CTTTGAGGAAGAAT	оу 1021 таатаатаатсста                    Db 2434 таатаатаатсста	Qy         961         ATCATTGTAACTAA           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Dy 901 AGAGCTTGTATGGT 	1	841 2254	781 2194 841 2254	721 2134 781 2194 841 2254	661 2074 721 2134 781 2194 841 2254	601 661 2014 2074 721 2134 781 2194 841 2254	541 601 2014 661 721 2134 781 2194 841	481 1894 1954 2014 2014 2074 721 2134 2134 2134 2134 2134	1834 481 1894 541 2014 661 2074 2134 2134 2134 2134 2134	421 483 1834 1894 541 2014 661 2074 721 2134 2134 841	361 1774 421 1834 481 1954 541 1954 661 2014 2014 2014 2134 2134 2134	301 301 361 1774 421 1834 481 1894 541 1954 541 1954 601 2074 661 721 2134 2134 22134	1654 301 361 1714 421 1834 481 1834 541 1954 601 1954 661 2014 661 2014 2014 2074 2074 2134 2134
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1654	241	1594	121 1534	61 1474	<u>i – i</u>	Query Match Best Local Similar: Matches 1387; Con		ORIGIN	ORIGIN	ORIGIN	CDS ORIGIN	D OBS	Ø	D ONCE ST	¢	e	Ф — — —	e [ ]]	e " ' 'j 'j

0y         301         CAACTAACTCAACTCAATTTTCCCTCATAGCAGCATTCCATCTTCCCGATCTTCTTGCT	OY 241 CAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 	Oy         181         CCACTAGAGGAATATAAATGTGTTAAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA           Db	OY 121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 	$ \begin{array}{c} Qy &  \  \  \  \  \  \  \  \  \  \  \  \  $	OY         1         AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC           0Y	Query Match 81.2%; Score 1385.8; DB 6; Length 2802 Best Local Similarity 99.9%; Pred. No. 2.2e-270; Matches 1387; Conservative 0; Mismatches 2; Indels 0;	-	/not /prod /db LINGG CITAL VVXA QSFPN QSFN VVXA QSFN VVXA	/organism="unidentified" /mol_type="unidentified" /db_xref="taxon:32644" 301415	BIOTECHNOLOGY AND BIOLOG SCIEN (GB) COMMENT Other publication AU 2317095 951129. FEATURES Location/Qualifiers source 1. 2802	30000-A 1.09-NO	NISM unidentifie	14 A47227 TION Sequence 1 from Patent WO9530000. ION A47227 N A47227.1 GI:2301257 DS unidentified	94 THCHGGTTCAT 2804 A47227 Sequence 1 from Patent WO9530000. A47227.1 GI:2301257 unidentified	881 TFCTGGTTCAT 1391 1	794 381 381 381 34 А4 А4	73 88 98 94 94 84 84 84	1
	CTATGGTTCTCCACTAT	СТААGGGCCCAGCCCT 	aattgattagaaaatge                    aattgattagaaaaatge	ACATTCTATGATCATTC                   ACATTCTATGATCATTC	AATTAACAGGGCCTCTC                   AATTAACAGGGCCTCTC	Length 2802; Indels 0; Gaps		GYLLSABCTVFLDHEN TRATERTTEFNKQYVDGI TRATERTTEFNKQYVDGI KNGRCEQPCKNSADNK KVAFDVNJVNSTEABET I GGSIVNBKWLVTAAHCJ LQYLKVFLVDBATCLRS GIISWGEECAMKGKYGJ					ar PAT	ar PAT	ar PAT	linear PAT 07-	linear PAT 07-	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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Qy 361 TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 		QY 241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300 	QY 181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240 	$ \begin{array}{llllllllllllllllllllllllllllllllllll$	$ \begin{array}{llllllllllllllllllllllllllllllllllll$	Qy         1         AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC         60           Db         1390         AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC         1449	Query Match 81.2%; Score 1385.6; DB 6; Length 2781; Best Local Similarity 99.7%; Pred. No. 2.4e-270; Matches 1388; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	GLHEGARDSCOGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRYVNWIK EKTKLT" ORIGIN	NOKSCEPAVPFPCGRVSVSOTSKLTRAEAVFPDUDY VNSTEAET I LDNI TOSTOSFND FTRVVGSEDAKEGOFPDOVLNGKUDAFCCGSI VNBKMI VTAAHCVETGVI TVNAGE HNI BETEHTEOKKUVI IR I I PHHNYNAAI INKYNHIDI ALLELDBEI-VLNSYVTPI CI ADK EYTNI FLEFGSGYVSGWGRVFHKCERSALVLOYLRVDLVDBATCLESTKFTI YNNMFCA	/dL_xref="GI:825656" /translation="MIMASSPGLITICLLGYLLSAECTVFLDHENANKILNRPKRYNS GKLEEPYQGNLEERSCMEEKCSFEEAREVFENTERTTEFMKQYVOGDQCESNPCLNGGS CKDDINSYECWCPFGFEGKNCELDVTCNIKNGTCEQFCKNSADNKVVCSCTEGYRLAE	CDS 211391 /codon start=1 /protein id="CAA01607.1"	/mol_type="unassigned RNA" /db_xref="taxon:9606" gene 21139" /gene="factor IX"	ë	REFERENCE 1 (bases 1 to 2781) AUTHORS Brownlee,G.G. and Choo,K.H. TITLE Molecular cloning of the gene for human anti-haemophilic factor IX JOURNAL Patent: BP 0107278-A 15 02-MAY-1984;	SOURAB ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buteria; Buarchontoglires; Primates; Catarrhini; Hominidae: Homo.	TTION H. sapiens factor IX mRNA. SION A22493 DN A22493.1 GI:825655 RDS .	RESULT 15 HSFACIXM LOCUS HSFACIXM 2781 bp RNA linear PAT 02-MAR-1995	

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h completed: April 18, 2006, 14:56:56 ime : 9359 94 acca	770 TTCTGGTTCAAA 278	ין אריירייעטאטאיזיזאריזטעריטעריטיריטיזיטיזיריריזיטיטאאוואאואטערטטטט 10 10 ייייייייייייייייייייייייייייייייי	ւս	{	ATAGTTA	0 GAGAAGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 264	201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1	1141         AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG         1200	2470 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG		1021 TAATAATAATGCTAACAGAAAGAAGAGAGAGCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080	961 ATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020 	2290 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTGACGAAGGCAAGATTGGCAT 2349	901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960	30 TATGCGTGTGTGTAGACACACACGCATACACACACATATAAAGGAAGCAATAAGCCATTCTA 2	41	781 ATATATATATATATATATATAAAATATATAAATATAAAATAT	111111111111111111111111111111111111	721 TGAAGTAAGGIGCCIGAAAAGTIIGGGGGAAAAGTIICITICAGAGAGTIAAGTIA	50 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGGGACTTGCTTTTCAGAACATAGGGA 2	661 CATGTCTATCAAACCCAGACTIGCTICCATAGIGGAGACTIGCTITICAGAACATAGGGA 720	601 CATUGTICETTAAAGAGAGAATGGGGAGCATCATTICTUTTATACTTCTUTACACACUTTATA 660 	30 CAAATCCCCAATCCCCCAAATCAGTTTTTCTCTTTCTTTACTCCCTCTCCCTTTTTACCCCTC 19	541 CAAATCCCCAATCCCCAAATCAGITITITCTTTCTTACTCCCTCCTCTCCCCCTTTTACCCCC 600	1870 AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1929	481 AAACTCATCAAAAAACACTACTCCTTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540	421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAGAACACAGGAGTAGCTCAGAGGCTA 480 

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RESULT 1 AAI71008 **WWXBX** XSX B ი The present sequence is that of the 3' untranslated region (3' UTR) of the human Factor IX gene. The 3' UTR, which includes a polyedenylation signal. It was incorporated into expression cassettes of the invention that were designed for liver-specific expression of Factor IX. The cassettes also include an hepatic locus control element, an hepatic promoter located 3' to the hepatic locus control element, a Factor IX Miao Nucleic acid construct for expressing nucleic acid molecules, proteins in mammalian liver cells, has operably linked hepatic locus control element, hepatic promoter, coding sequence, polyadenylation signal and intron. Pactor IX; human; expression cassette; gene therapy; 3' untranslated region; 3 WPI; 2002-114582/15. 20-JUN-2000; 2000US-0212902P Homo sapiens. Human Factor IX gene 3' untranslated region. 18-MAR-2002 AAI71008; AAI71008 standard; DNA; 1707 promoter Example 1; Page 57-59; 64pp; English. (STRD ) UNIV LELAND STANFORD JUNIOR. (UNIW ) UNIV WASHINGTON. 19-JUN-2001; 2001WO-US019634. 27-DEC-2001. WO200198482-A2 203.8 200.6 200.6 200.6 172.6 172.4 159 159 159 Ê Kay MA; 774.4 774.4 773.9 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 774.4 774.4 774.4 774.4 773.9 774.4 774.4 773.8 774.4 773.8 773.8 774.4 773.8 773.8 774.4 773.8 773.8 774.4 773.8 773.9 774.4 773.9 774.4 773.9 774.4 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 773.8 774.7 774.7 774.7 774.7 775.8 775.9 775.8 775.9 74.5 74.5 74.5 10.1 (first entry) ; expression cassette; liver; untranslated region; 3' UTR; 422 1610 13928 1548 1548 1548 1438 1438 1638 1639 1612 1971 1273 1273 1272 1275 1275 1276 1639 1272 201 201 201 AAQ81549 AAQ76017 AAX88292 ABX47596 AAX88061 AAH77500 AAN50362 ADH42200 ADQ40547 ADQ40547 ADQ40266 ADQ40829 ADQ40829 AAN50351 AAN50049 AAF54080 AAF54073 AAF54073 AAF54075 AAF54079 AAF54079 AAF54079 AAF54077 AAF54077 AAF54078 ABA55251 ABA55251 ABA55251 ABA552575 ABQ82328 BP. ALIGNMENTS

Aaf54077 hPIX gene Aaf54078 hPIX gene Aba55251 Human foe Aba28575 Human liv Abg83328 Human NOV Adh42196 Novel hum Aan50049 Sequence Aan50362 Sequence Adh42200 Novel hum Adq40547 Myocardia Adq4086 Myocardia Adq4086 Myocardia Adq41116 Myocardia Aax88061 Aah77500 Aaq81549 Aaq76017 Aaf54075 Aaf54076 Aaf54074 Aaf54073 Aan50362 Aax88292 Aan50351 Aaf54079 Abx47596 Aa£54080 Bovine ES L Human IGF D Haemophil Pactor-IX hFIX gene hFIX gene hFIX gene hFIX gene hFIX gene hFIX gene Human Pac Human Fac Sequence Human

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CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACATGGTGACATAGGGA       720       RESULT         [	ANACTCATCATCANAACACTACTCCTTTTACCCTCAACCTTTTACCTTTT       540         DIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TCTCCCAACCAAAACATCAATGTTTAATTAGTTCTGTATACAGGTACAGGATCTTTGGTCTAC       420       Oy	CMAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300     CY       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TTTTCTCTTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATGGAA 180 D 	AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGCCCTCTCAC     60     D	coding sequence, and an intron (see AAI71003-16). Also provided are vectors that include an expression cassette of the invention. These may episomal or integrating vectors, including viral vectors, and are used in a claimed method of ameliorating disease. A therapeutic amount blood 
TLT 2 AAF54018 standard; DNA; 38059 BP. AAF54018; 30-MAR-2001 (first entry) Human factor IX (hFIX) gene, SEQ ID NO:4. Age-related gene regulation; liver-specific; gene expression; human factor IX; hFIX; AE5'; AE3'; age-regulatable expression construct;		1441 TGATGATGGAGGACTACTGACAAATCACTGACCAGCTGACCAAGCTGCTGCCTTCTCC 1500 1441 TGATGATGCATGGGACTACTGACCAAAATCACTGTGACCCTGCCAAGCTGCTGCCTTCTCC 1500 1441 TGATGATGCATGGGACTACTGACAAAATCACTGTGACCCTGCCAAGCTGCTGCCTTCTCTCC 1500 1501 TGCCCCAACCTCACGCCCGGGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTAGTC 1560 1501 TGCCCCAACCTCACCCCCAGGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTAGTC 1560 1501 TGCCCCAACCTCACCCCCAGGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTGGCTGG 1620		GALAAGGGTGCAGGGCTCAAAGGCATTAGTTCCAATTCCAAGCGAGCG	CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGGAGCAAGAAGTTGA 	TATGCGTGTGTGTGTAGACACACACACATACACACATATAATGGAAGCAATAAGCCATTCTA 

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The invention relates to mucleic acid sequences which regulate gene crossing the invention identifies regions of the human factor IX (hFX) gene, and a region of the human protein C (hC) gene, which are age-related cregulatory sequences. The hFX age-related regulatory sequences are designated AES' (AFS4018) and AS' (AFS4017), and are found in the 5' (TRR (at position 2164-2165 of AFS4018) and AS' (article appression) creating the position 2164-2165 of AFS4017) and are found in the 5' (article appression) and correct effects on hFX mRNA and AS' acting to increase hFX creating to stabilise hFX mRNA, and AS' acting to increase hFX creating the construction of recombinant expression. The creating the construction of recombinant expression of a desired sequence in an age-related regulatory sequences can independently exert effects on hFX mRNA and AS' acting to increase hFX creating to increase in an age-related regulatory sequences of the invention, along with their homologues, variants and fragments, may creating the construction of recombinant expression vectors for the expression vectors include those encoding proteins involved in a host creating the protein c and antithrombin III, human alpha-1-creant the spe promoter. The expression vectors of the invention may be used in gene the spe promoter. The expression vectors of the invention may be used in gene the spe promoter. The expression vectors of the invention may be used of such age-related conditions such as thromboil, cancer, creating and use expression. Transgenic such as thromboil, cancer creating and gene expression reagenes, in screening for conditions associated with the natural age-related rise in factor IX creating and gene expression reagenes, in screening for creating and gene expression. Transgenic calls or animals that contain vectors of the creating and gene expression sequences in screening for contain the specific agents and for studying normal processes such as eappression are useful as a models of these theases, in screening for contain the s Query Match Best Local Similarity Matches 1703; Conserv The invention relates expression in an age--The invention antisense therapy; gene therapy; thrombosis; cardiovascular disease; diabetes; Alzheimer's disease; Parkinson's disease; cancer; osteoporosis; osteoarthritis; dementia; ds. New regulatory elements that control age-related in gene therapy and for reducing Factor IX expres WPI; 2001-061708/07. P-PSDB; AAB60281, AAB60282, AAB60283, AAB60284, AAB60285, AAB60287, AAB60288, AAB60289 09-JUN-1999; 06-JUN-2000; Homo sapiens Disclosure; WO200075279-A2 Sequence 38059 UNIV MICHIGAN Fig 8A-B; Kurachi 2000WO-US015728 BP; 99US-00328925 12326 ŝ 99.7%; 99.9%; 225pp; English. A; 7397 Score 1701.8; Pred. No. 0; id. No. 0; Mismatches <u>.</u> 7441 G; elated gene expression. 멻 10895 4; Τ; Length 38059; 0 expression, useful G AAB60286 0 Other, Ś 昂 昂 8 뎡 ą 昂 Ş 昂 Ş 昂 Ş 문 Ş 뮿 8 昂 Ş 昂 Ş 뮹 Ş 昂 8 昂 Ş 昂 8 昂 Ş 昂 Ş 망 Ş 昂 Ş 35053 34933 34813 34753 34633 34573 34393 35353 35293 35173 35113 34993 34873 34693 34513 34453 34333 35233 1021 301 601 541 481 421 361 241 181 121 196 106 841 721 661 781 £ ... CAACTAACTCACTCAATTTTCCCCTCCTTAGCAGCATTCCATCCTTCCCGATCTTCCTTTGCT AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAAATTGAAAAATTAACAGGGCCCTCTCAC CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTC AAACTCAACAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGGACAGGATCTTTGGTCTAC CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG CCACTAGAGGAATATAATGIGITAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180 TAACTAATCACTTTCCCATC TAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412 TAATAATAATGCTAACAGAAAGAAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 1080 ATCATTGTAACTAAAAAAGCTGACATTGACCCCAGACATATTGTACTCTTTCTAAAAAATAA 1020 AGAGCTTGTATGGTTATGGAGGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT TATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA TATGCGTGTGTGTGTAGACACACACACACACACATATAATGGAAGCAATAAAGCCATTCTA 900 CATGTCTATCAAACCCAGACTTGCTTCCCATAGTGGAGACTTGCTTTCCAGAACATAGGGA 720 CAAATCCCAATCCCCAAATCAGTTTTTCTTTCTTACTCCCTCTCCCTTTTACCCTC TCTATCACAAGGCCAGTACCACACTCATGAAGAAGAACACAGGAGTAGCTGAGAGGCTA TCTATCACAAGGCCAGTACCACACACTCATGAAGAAGAACAAGGAGGAGTGAGGGCTGAGAGGCTA 480 CCACTAGAGGAATATAATGI ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA GTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 420 360 300 . 34572 096 35172 34932 600 540 34812 34752 34692 240 34452 60 35052 34872 34632 34512 35352 35232 35112 34992

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(GENE-) GENE LOGIC INC. Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;	2000; 2000US	APR-2002.		, liver cancer; ds; hepatocell static liver tumour; cytostati se progression; drug toxicity	13-AUG-2002 (first entry) Gene #2125 used to diagnose liver cancer.	ABN95627 ABN95627 standard; DNA; 38059 BP. XX AC ABN95627:	013	35953 GCCCAGTGGCTCACGCCTATATATCCCCAGCACTTCTGGAGGCCCAAGGTGGGCGGATCACCT 36012 1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705	35893 AATATATTTTTGTCTTCGCATATAAGTATAAGTATAAACATATTTTTAAATTTCTTGGCTGG 35952 1621 GCCCAGTGGCTCACGCCTATAATCCCCAGCACTTCTGGAGGGCCAAGGTGGGCGGATCACCT 1680		1501 TGCCCCAACCTCACCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTTAGTC 15	1441 TGATGATGGAGAGACTACTGAGAAAATGACTCTGAGCCTGCCAAGCTGCGGCGTGCCTTCTCC 1500	1381 TICIGGITCATACCITGGCITTIIGIGGATICCATIGAIGIGAAICAGICACCIGIAIT 1440 	1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380 	1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320 	1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260 	35473 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 35532	35413 CTTTGAGGAAGAATTCAACAGTGTGTGTGTGAGCAGGGAGGCAAGCAA	CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG
8 8	B &	Qу Db	B 8	5 Q	, DP V	dd Ag	р Q	р <i>2</i>	р Q	₽ Ş	3.00	QS	ž888	3888	8888	8888	XX PS XX	PT	DR
601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGGTTATA 660 	541 CAAATCCCAATCCCCAAATCAGTTTTTCTTTTTTTTTACTCCCTCTCTCCCTTTTACCCTC 600 	481         AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC         540           1	421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480 	361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 	301 CAACTAACTCAACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCCTTTGCT 360 	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300 	181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240 	121         TITTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATGATTAGAAAATGGAA         180	61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120 	1 AALGAAMAA KOATTICCAAGGITAATTCATTGAAATTGAAAATTAACAGGGCCTCTCAC		Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other; uery Match 99.7%; Score 1701.8; DB 6; Length 38059;	for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences	liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well a markers that can be used to monitor disease states, disease progression drive forgistive drive officary and drive metabolism. Note: The secuence of	expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastat	The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of	Claim 1; SEQ ID NO 2125; 298pp; English.	Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.	WPI; 2002-426119/45.

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97         661         CARTECTARCOARCCOARGCTTRGCTTCCARAGEAGACTTGCTTTCCARAGEAGTTTCCARAGEAGTTTCCARAGEAGTTTCCARAGEAGTTTCCARAGEAGTTAGAGTTCCATACAGAGTTAGAGTTCCATACAGAGTTAGAGTTCCATACAGAGTTAGAGTTCCATACAGAGTTAGAGTTCCATACAGAGTTAGAGTTCCATACAGAGTTAGAGTTCCATACAGAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGTTAGAGTTCCARAGEAGTTAGAGTTCCARAGEAGTTCCARAGAGTTCCARAGEAGTTCCARAGAGTTCCARAG
3 3 3 4 9 9 3 7 2 1 7 6 6 1 7 3 3 5 1 3 3 5 1 7 3 3 5 1 7 3 1 7 6 6 1 7 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 3 5 1 7 7 3 5 1 7 7 3 5 1 7 7 3 7 1 7 7 7 3 7 1 7 7 7 7 7 7 7 7
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661 34993 721 35053 781 781
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661 CATGTCTATCAAACCCAGACTTGCTTC 

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1 AATCAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAAQAGGCCTCTCAC 60 	Query Match 99.7%; Score 1701.8; DB 10; Length 38059; Best Local Similarity 99.9%; Pred. No. 0; Matches 1703; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Sequence 38059 BP; 12326 A; 7397 C; 7441 G; 10895 T; 0 U; 0 Other;	aimed human gene sequence which is used in the exemplicesent invention.	he methods are useful for tre patitis or cirrhosis. The pi	he expression rever in crace of our of the progression of the progression and the progression of the progres	method for using the computer system to present information ident	igonucleotides; (10) a computer system comprising a can formation identifying the level in liver tissue of a s	y of the genes; (9) a solid support comprising the at least two	ogression of liver cancer; (8) a composition	ncer related to chronic hepatitis from liver rehated to chronic hepatitis (7) screening for an agent capable (	tient with chronic hepatitis or cirrhosis; (6) differentiating liver	reating a patient with liver cancer; (4) typing a liver disease in a reacting a patient with liver cancer; (4) typing a liver cancer in	BO described: (1) detecting the progress	here differential expression of the genes is indicative of 1	ills comprising detecting the level of expression in a tissue sam to or more genes given in the specification (see ADD70997 to ADD7	ne present invention describes a method for diagnosing liver cancer	Claim 1; SEQ ID NO 102; 176pp; English.	yvel of expression in a tissue sample of one or more genes assoc th cancerous liver tissues.	agnosing liver cancer cells, useful for treating liver can sociated with chronic hepatitis or cirrhosis comprises det	1; 2003-663343/62.	Koh SS, Liu Q, Chung H, Zeng W, Lee B, Yeramilli S, Song SY;	(GENB-) GENE LOGIC INC. (LGBI-) LG BIOMEDICAL INST.	21-DEC-2001; 2001US-0341815P. 31-DEC-2001; 2001US-0343185P.	20-DEC-2002; 2002WO-US040718.	31-JUL-2003.	W02003061564-A2.	Homo sapiens.	liver cancer; chronic hepatitis; cirrhosis; liver disease; hepatotropic; cytostatic; gene therapy; human; gene; ds.	Human coagulation factor IX gene SEQ ID NO:102.	15-JAN-2004 (first entry)	AD071098;	ULT 4 71098 ADD71098 standard; DNA; 38059 BP.	

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961       ATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA       1020         35293       ATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA       35352         1021       TAATAATAATGCTAACAGAAAGAAGAAACCGTTCGTTTGCAATCTACTACTACTAGTAGAGA       1080         35353       TAATAATAATGCTAACAGAAAGAAGAAACCGTTCGTTTGCAATCTACAGCTAGTAGAAGA       1080         35353       TAATAATAATGCTAACAGAAAGAAGAAACCGTTCGTTTGCAATCTACAGCTAGTAGAAGA       15412         1081       CTTTGAGGAAAGAATCAACAGTGTGTCTTCAGCAGTGTTCGAAGCCAAGCAAG	61 93 21 221 23 53 53 53 73 73 33	61       TAACTAATCACTTTCCCATCTTTIGTTAGATTTAGATTTGAATATAACATTCTATGATCATTGT       1.20         34393       TAACTAATCACTTTCCCATCTTTIGTTAGATTTGAATATAACATTCTATGATTAACATTCTATGT       1.20         34393       TATCTCTTTACAGGGAAGAATTTCATATTTAACTTGAAGGAAATTGAATAACATTCTTTGT       3452         34453       TTTTCTCTTTACAGGGAAGAATTTCATATTTAACGTCAAGGCAAATTGAATAACATTGGAA       34512         34513       CCACTAGAGGAAATTTCATATTCTCAAGTAACTACAGTCAATTGAATAAAATGGAA       34512         34513       CCACTAGAGGAAATTTCTCCAACTCTCCAACTCAAGTCAATTGAATAAAATGGAA       34512         34513       CCACTAGGGAAATTTCTCCAACTCTCCAACTCAAGTAATTCTAAGGGCCCAGGCCCTTGA       34572         34513       CCACTAGGGAAATTTCTCCAACTCTCCAACTCAATACAATACAATTCAATAGGTCTCCAACTAAGGGCCAACTCAATTGCAATAGGGCCAACTCAATGTTCTCTTAAGTCTCCAACTAACT
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16-1 16-1 (CH: (UYN (UYN (UYN (UYN) (UN) (UN) (UN) (UN) (UN) (UN) (UN) (U	<pre>LT 5 4034 AAA54034 standard; DNA; 2775 BP. AAA54034; 08-FEB-2001 (first entry) Human factor IX coding sequence. Vitamin K dependent protein; VKDP; gamma-carboxylation; chimeric protein; fusion protein; coagulation factor; Factor X; Factor VII; Protein S; Factor IX; Protein C; prothrombin; blood clotting; haemophilia; human; ds. Homo sapiens. W0200054787-A1. 21-SEP-2000.</pre>	35473       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCCTTTTACCCCTC 600	481         AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC         540	1005 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1864	421 TCTATCACAAGGCCAGTACCACCACTCATGAAGAAAGAACACAGAGGAGTAGCTGAGAGGGCTA 480	361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 	301 CAACTAACTCAACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 1744	ראיז איז איז איז איז איז איז דער דער איז איז איז דער גער איז גער איז ער איז	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 300	151 CLACHARMONAN ANALOLUL AND		121 TTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATGGAA 180	61 TAACTAATCACTTTICCCATCTTTIGTTAGATTTGAATATATACATTCTATGATCATTGCT 120 	1 AATGAAAGATGGATTTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 1444 		Query Match 81.5%; Score 1391; DB 3; Length 2775; Beet Local Similarity 100.0%; Pred. No. 2.66-289; Thalla D. Gang D	Sequence 2775 BP; 859 A; 528 C; 564 G; 824 T; 0 U; 0 Other;	propeptide sequences (modified or not) and VKDP's. This sequence encodes the signal, propeptide and mature protein sequence of human Factor IX	alleviating a VKDP associated disease. The fusion constructs result in the production of fully gamma-carboxylated mature VKDPs, which are biologically active The invention encompasses all combinations of	carboxylation of a VKDP to produce a fully gamma-carboxylated VKDP. The fusion proteins and recombinant cells expressing them are useful for	nucleic acid sequence encouring a vicanin A-respensed, proteins encoded are vitamin K-dependent protein gamma- carboxylation enhancers and are useful for optimising the gamma-	production of biologically active factor Arra. Bolaced conmerce polymucleotides are described which encode a propeptide fused to a	of the signal sequence, propertide, internal tripeptide and full gamma- carboxylation are all steps which are important requisites for the	removal of an internal tilpepting to yield two-timent actors and tensors of the propeptide just prior to secretion. While some of these modifications do not appear essential for factor X function the removal	tirgt epidermal growth factor (kGF) domain to beca nyuroxyaspartic actu; addition of N- and O-linked oligosaccharides to the activation peptide;	disulfide bonds; modification of amino terminal glutamic acid residues, to gamma-carboxyglutamic acid; modification of one aspartic acid in the	Bfficient processing and release of mature two-chain factor X into the circulation requires: removal of the signal sequence; formation of	Disclosure; Fig 6Di-ii; 60pp; English.		protein useful for treating diseases associated with the protein,	
													<u> </u>		<u> </u>														
KW	XX XX	X R i	X A X	RESULT ( ABV77053 ID ABV	Dр	ş	00 0	5 5	ş	B 7	5 8	र्छ -	ş	DD 2	<b>१</b>	B 8	Db .	ş	B 7	5 5	ş 8	Db	Q	Dp	ş	윤 1	<b>Q</b>	PH	
	Nucleotide sequence of human Factor IX. Factor VIII; non-viral vesicle vector; vesicular membrane; hepatitis B;	(first entry)	ABV77053;	LT 6 7053 ABV77053 standard; DNA; 2804 BP.	2765 TUCTGGTTCAT 2775	1381 TTCTCGCTTCAT 1391	 	2645 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTAATGTTAATCCTTCTATCTTGAAT 2704 1331 CTTCTAGGTTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380	1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320	2585 GRGAAGGGTGCAGCACGACTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2644		2465 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	05 TAATAATAATGATAACAGAAAGAAAGAAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA	21	961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTTCTAAAAATAA 1020 		901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960	2225 TATGCGTGTGTGTGTGTGTGAGACACACACACGCATACACACAC	41 TATGCGTGTGTGTGTGTAGACACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA	781 ATATATATATATATATATATAAAATATATAATATATAT		721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	2045 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 2104	661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720	1985 CATGGTCGTTAAAGGAGAGAGGAGGAGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2044	2	1925 CAAATCCCCAAATCACTTTTTCCCTTTCTTACTCCCTCTCCCCCTTTTACCCCTC 1984	•

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RESULT 7 AAX28626 ID AAX28626 standard; DNA; 2792 BP. XX AC AAX28626;	Oy       361       TCTCCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC       420         Db       1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/
Db 2794 TICTGGTICAT 2804	Oy         301         CAACTAACTCAACTCAATTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT         360           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
2734	Oy         241         CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG         300           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
1261 TTTCTGGTTTCGTGTTCACCAPGGAACATTTTGATTAATGCTTATCTTGAAT 	Oy         181         CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGGCCCTTGA         240           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
1201 GAGAAGGTIGCAGCATGAAGGCATAAGTCATTCCAATTCCACCAACTAAGTTGTCCT 	Oy 121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180 
1141 AGTIGCCTAGACCAGAGAGACATAAGTATCATGTCTCCTCTTAACTAGCATACCCCGAAGTG 	$ \begin{array}{llllllllllllllllllllllllllllllllllll$
101 CTTTGAGGAAGAATTCAACAAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	Qy         1         AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC         60           Db         1414         AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAAATTAACAGGGCCTCTCAC         1473
1021 TAATAATAATGCTAACAGAAAGAAGAAGAGACATCGTTCGT	Query Match 81.5%; Score 1391; DB 8; Length 2804; Best Local Similarity 100.0%; Pred. No. 2.6e-282; Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2374 ATCATTGTAACTAAAAAAGCTGACATTGACCCCAGACATTGTACTCTTTCTAAAAATAA	
.961	
Cy 901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960	CC are used to construct non-viral vesicle vectors. These vectors comprise a CC vesicular membrane with hepatitis B envelope protein exposed on the CC vesicle surface, and a nucleic acid expression construct comprising a
DY 841 TATGUGTGINGTGAGACACAGAGGGATACACACATATAATGGAAGCAATAGGCATTCTA 900	Disclosure; Page 19-21; 34pp; English. The present semience encodes a human Pactor IX Pactor IX polynucleatide
781 ATATATATATATATATATATATATATATATATAATATAATAT	PT New non-viral vesicle vector comprises vesicular membrane with hepatitis PT B envelope protein and nucleic acid expression construct comprising PT complete factor VIII or IX coding sequence, useful for treating PT hemophilia.
Dy 721 TGAAGTAAGETGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTATTTT 780	XX DR WPI; 2003-093125/08. DR P-PSDB; ABB99529. XX
CATGTCTATCAAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA	PI Chien KR, Hoshijima M;
QY 661 CATGICTATCAAACCCAGACTIGCTIGCTIGGAGACTIGCTITTCAGAACATAGGGA 720	23-APA-2001;
2014 CATGGTCGTTAAAGGAGAGATGGGGGGGGAGCATCATTCTGTATACTTCTGTACAACAGTTATA	25-APR-2002;
Db 1954 САЛАТСССААТССССАААТСАСУТТТТСТСТТТСТТАСТСССТСТСТСССТТТТАССССТС 2013 Ом 601 сатестосттааассаасасаасаасаасаасаасаатсаттсттатасттстстстасасасаттата 660	XX PD 31-OCT-2002. XX
	WO200286091-A2.
Oy         481 AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC         540	PH Key Location/Qualifier8 PT CDS 30.1415 PT /rtag= a PT /product= "Pactor IX"
Db 1834 TCTATCACAAGGCCAGTACCACCACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 1893	XX OS Homo sapiens. XX

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ΟΥ 241 C Db 1642 C	QY 181 C Db 1582 C	Qy 121 T Db 1522 T	Qy 61 T   Db 1462 T	Qy 1 A   Db 1402 A	Query Match Best Local Si Matches 1389;		CC Factor IX-RJ CC Pactor IX-RJ CC Pactor Xa in CC Factor Xa in	Disclos		WPI; P-PSI	Staffor	(UYNC-) (STAP/) (CHAN/)	XX PR 21-JUL-1997;		PN WO9903496-A1 XX PD 28-JAN-1999.		PH Key PT CDS PT	OS Homo sapiens. OS Synthetic. YY			XX DT 07-JUN-1999 XX	
CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 300 	CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTCTAAGGGCCCAGCCCTTGA 240 	TTTTCTCTTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTACAAAATGGAA 180 	TAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATAT	AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60 	arch 81.3%; Score 1387.8; DB 2; Length 2792; al Similarity 99.9%; Pred. No. 1.2e-281; 1389; ConBervative 0; Mismatches 2; Indels 0; Gaps 0;	oding Factor IX can be used to facilitate blood clotting, e.g. ts afflicted with haemophilia B 2792 BP; 858 A; 541 C; 569 G; 824 T; 0 U; 0 Other;	Factor IX-R338A protein having an amino acid substitution at amino acid position 338 of arginine to alanine. Factor IX converts Factor X to Pactor Xa in the mammalian blood coagulation cascade, in a process that requires a phospholipid surface, calcium ions and Factor VIIIa. Nucleic	26-32; 38pp; English.	Pactor IX antihemophilic factor with increased clotting activity - due to an amino aid substitution (of arginine) at position 338.	1999-131867/11. 38; AAYO3203.	DW, Chang JL;	UNIV NORTH CAROLINA. STAFFORD D W. CHANG J L.	7; 97US-0053571P.	8; 98WO-US014750.	9. Al.		Location/Qualifier8 1561423 /*tag= a	<b>D9</b> .	Human; Factor IX-R338A; substitution; Factor X; Factor Xa; mammalian blood coagulation cascade; phospholipid surface; calcium ion; Factor VIIIa; blood clotting; haemophilia B; ss.	sequence of human factor IX-R338A.	9 (first entry)	
5 B 7	5 B 1	\$ F 1	\$ B 1	8 B 1	5 B 1	8 B 8	5 20	윰 7	8 B	8	88	? 문 !	\$ I	7 2	Dþ	Q	5 Q	망	8 8	Ş	90 97	
TICIGGTICAT 1391	•					961 ATCATTGTAACTAAAAAAGCTGACATTGACGTCCGAGACATATTGTACAGCTAGTAGAGA 1080 			2182 ATATATATATATATATATATATAAAATATATAATATA		212 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC			601 CATGGTCGTTAAAGGAGAGAGAGGAGGAGGAGCATCATCTGTTATACTTCTGTACACAGTTATA		541 CAAATCCCCAATCCCCCAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCT	481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 		1762 TCTTCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 421 TCTATCACAAAGGCCAGTACCACACCACATGAAGAAAGAA	361 TCTCCAACCAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTA	301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT	• •

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TTTTCTCTTTACAGGGGAGAAITTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA	61 TAACTAATCACTTTCCCATCTTTGTTAGATTGAATATAATACATGCTATCATGATCATGCT 120 	1 AATGAAAGATGGATTTCCAAGGTTAATTCGATTGGAAATTGAAAATTAACAGGGCCTCTCAC 60 	Query Match     81.2%; Score 1385.6; DB 1; Length 2781;       Best Local Similarity     99.7%; Pred. No. 3.6e-281;       Matches 1388; Conservative     0; Mismatches     4; Indels     0; Gaps     0;	Correct PA field.) Sequence 2781 BP; 859 A; 526 C; 567 G; 829 T; 0 U; 0 Other;	clone lambda HIX-1) deposited as NCIB NO. 11749; Recombinant DNA in which the cloning vehicle is the modified pAT 153 plasmid present in E.coli NCIB NO. 11747; Recombinant DNA in which the bovine factor IX DNA sequence is contained in the recombinant DNA transformed into E.coli to	The inventors claim DNA molecules comprising part or all of the human factor IX DNA. The invention also includes cDNA derived from human factor IX RNA. Specifically claimed are: recombinant DNA (the phage present in	Recombinant DNA cloning vehicles - useful in prodn. of factor IX polypeptide and of diagnostic probes for Christmas disease.	WPI; 1984-049331/08. P-pSDB; AAP40178.	(NATR ) NAT RES DEV CORP. (BROW/) BROWNLEB G G. Brownlee G, Choo KH;	04-AUG-1982; 82GB-00022485. 06-MAY-1983; 83GB-00012491.	16-FEB-1984. 03-AUG-1983; 83WO-GB000191.	mat_peptide 1441391 /*tag= b WO8400560-A.	peptide 21. /*ta	Christmas disease; therapy; haemophilia; factor IX; blood clotting; diagnosis; ss. Homo maniens	8	25-MAR-2003 (revised)	, pruntata, com, 2001	RESULT 8 AAN40142 ID AAN40142 standard. CDNA. 2781 RD	2782 TICHGITCAT 2792
Ŷ	В 8	Db VY	8 B Q	9 0 QY	da da	40 V	р С	DP QA	5 Q	8 S	DP QY	Qу рь	4d Að	5 g	06 Q	2 Db	ş	р Х	۵D
1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260	1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200 	CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTCAGAGCCCAAGCAAG	TAATAATAATGATAACGAAAAAGAAGAAGAACCGTTCGTT	ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 	AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 	841 TATECETETETETAGACACACACACCACATATAATEGAAGCAATAAGCCATTCTA 900 	781 ATATATATATATATATATATAAAATATATATATATATA	721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	61 CATGTCTATCAAACCCAGACTTGCTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGA 	601 CATGGTCGTTAAAGGAGAGAATGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 660 	CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCCTTTACCCTC 	481         AAACTCATCAAAAACACTACTCCTCTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC         540	421 TCTATCACAAGGCCAGTACCACACATCATGAAGAAGAACACAGGAGTAGCTGAGAGGCTA 480 	361 TCTCCAACCAAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 	301 CANCINACTORITITICCTOTIAGENGCATCOATCTCCGATCTCTTTGCT 300 	30 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCAATCAGATACTAIGGTTCTCCACTATGG	241 CAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 300	181         CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA         240	1510 TTTTCTCTTTACAGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1569

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SQ	ХX	88	88	383	N RS	X PJ	33	첯뭪3	223	X PA X	PRX	ŖX	3 X	PN XX	PT	FT	33	33	33:	33	₩¥ \$	žX	2 2 2 X	DBX	RX	18 X	AAT02460 ID AAT	RESULT	B	ş	Db	ধ	50	Ş	昂
Sequence 2802 BP; 864 A; 537 C; 571 G; 0 T; 830 U; 0 Other;	s may also be used in gene therapy	or these sites removed, so as to reduce or prevent the effects of aberrant splicing and to increase FIX yields e.g. in milk. The improved	pressed in transgenic animals. Improved FIX sequences have at 1	Human Factor-IX (FIX) mRNA (AAT02460) includes cryptic donor and acceptor aites that cause a delation of 462 nucleotides from FIX constructs	Disclosure; Fig 2I-2II; 28pp; English.	mammary glands, and for gene therapy of haemophilia.	DNA expressing human factor IX having altered cryptic splice site - to ensure high level expression of protein in transgenic hosts, esp. in	WEI; 1995-393074/50.	Clark AJ;	(BIOT-) BIOTECHNOLOGY & BIOLOGICAL SCI RES COUNC.	03-MAY-1994; 94GB-00008717.	02-MAY-1995; 95WO-GB000996.	09-NOV-1995.	W09530000-A1.		/note= "base 1085 is the cryptic donor site" misc_feature 1547	<u>A</u>			_peptide	nome septens. Kev Location/Qualifiers	ant ana	<pre>Pactor-IX; haemophilia; gene therapy; transgenic animal; transgenic mouse; milk; cryptic splice site; PCR; primer; polymerase chain reaction; ss.</pre>	Human Pactor-IX mRNA.	15-APR-1996 (first entry)	AAT02460;	460 AATO2460 standard; mRNA; 2802 BP.	ΥΥ 90 	2770 TTCTGGTTCAAA 2781	1381 TICIGGITICATA 1392	2710 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 2769	1321 CTTCTAGAGAGTTGCTGGACCAACTGACGTATGTTTCCCCTTTGTGAATTAATAAACTGGTG 1380	2650 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 2709	1261 TTPCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320	2590 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTTAGTTGTCCT 2649
	뮹	8	뮹	Ŷ	망	Ŷ	5 B	Q Q	Db	8	망	Ŷ	Db	Q	Db	ş	Db	ş	рр d	ę	DB 2	Ş	B 8	망	Ŷ	DP	<i>२</i>	망양	}	8 4	5 8	3	Mar	Best	>
	2374 AUCAUUGUAACUAAAAAAGCUGACAUUGACCCAGACAUAUUGUACUCUUUUCUAAAAAAUAA 2433	961 ATCATTGTAACTAAAAAAGCTGACATTGACCCCAGACATATTGTACTCTTTTCTAAAAATAA 1020	2314 AGAGCUUGUAUGGUUAUGGAGGUCUGACUAGGCAUGAUUUGACGAAGGCAAGAUUGGCAU 2373	901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960			94 AUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAUAU	781 ATATATATATATATATATATAAAAATATATATATATAT		721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	2074 CAUGUCUAUCAAAACCCAGACUUGCUUCCAUAGUGGGGACUUGCUUUUCAGAACAUAGGGA 2133	661 CATGTCTATCAAAACCCAGACTTGCTTCCATAGTGGAGAGACTTGCTTTTCAGAACATAGGGA 720	2014 CAUGGUCGUUAAAGGAGAGAGAGGGGGGGGGGGGGGGGG	601 CATGGTCGTTAAAGGAGAGAGGGGGGGGGGGGGGGGGGG	1954 CAAAUCCCCAAUCCCCAAAUCAGUUUUUCUCUUUCUUACUCCCUCUCUCCCCUUUUACCCUC 2013	541 CAAATCCCCAATCCCCAAATCAGTTTTTTCTCTTTTTTTT	1834 AAACUCAUCAAAAAACUCCUUUUCCUCUACCUAUUCCUCAAUCUUUUACCUUUUC 1953 1834 AAACUCAUCAAAAAACUCCUUUUCCUCUACCUAUUCCUCAAUCUUUUACCUUUUC 1953	481 AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTTC 540		421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAGAAGAACACAGGAGTAGCTGAGAGGCCTA 480		361 TCTCCAACCAAAACATCAAIGTTTATTAGTTCIGTATACAGTACAG	301 CHACTAACTCAACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCCTTTGCT 360     :   :   :   :   :  :  :       ::	1654 CAAAAAUUGUGAAGUUAAAUUCUCCACUCUGUCCAUCAGAUACUAUGGUUCUCCACUAUGG 1713	241 CAAAATTGTGAAGTTAAATTGTCCACTGTGTCCATCAGATACTATGGTTCTCCCACTATGG 300	1594 CCACUAGAGGAAUAUAAUGUGUUUAGGAAAUUACAGUCAUUUCUAAGGGCCCAGCCCUUGA 1653	181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGGCCCTTGA 240	1534 UUUUCUCUUUACAGGGGAGAAUUUCAUAUUUUACCUGACCAAAUUGAUUAGAAAAUGGAA 1593	2	;   :  :  ::::   :  ::::  :::   ::::   ::::	י ב	1414 AARAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		cal Similarity 68.1%; Pred. No. 7e-281; cal Similarity 68.1%; Pred. No. 7e-281; cal Concernative 440: Migmatches 3: Indels	0 

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GB2125409-A.	exon	exon	exon	exon	mat_peptide exon		Homo sapiens. Key siq peptide	Part of the se Haemophilia;.C	992 992	AAN40177 ID AAN40177 standard; XX AC AAN40177;	ULT 10		1321 CTTC1  :: : 2734 CUUCU	1261 TTTCT ::: : 2674 UUUCU	2614 GAGAP		1141 AGTTC   ::  2554 AGUUC				1021 TAAT!
	n 2n	/*tag= 9 /label= x 729. 843 /*tag= h	ุ่ง ก	/label= u /label= u /*tag= e /*tag= v	ംധ	/*tag= a 94257 /*tag= c /label= t	Location/Qualifiers	sequence of human factor IX cDNA. Christmas disease; diagnosis; treatment; ss.	(revised) (first entry)	dard; CDNA; 2781 BP.				TTTCTGGTITCGGTGTTCACCARGGAACATTTGATTARAGTAATCCTTCARCTTGART 1320 ::: : :::  :::  : ::   : UUUCUGGUUUCGUGUCACCAUGGAACAUUUUGAUUAABGUUAAUCCUUCUAUCCUUGAAU 2733			AGTIGGCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATAGCCGCGAAGTG 1200		CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG		таатаатаатастаасаадаадаадаадасаарссттесстветасадствение 1090
DP QA	5 B Q	<u>ନ</u> ୪	5 5 2	р <i>б</i> у	B 8	55 Q	55 <del>6</del> 5	8 Q	р, Q	Qu. Ma	SQ	×88888	នននន	XSX	멁 멁 X	뒷둯	XPX	PA	PR PR	PFX	9
541 CAAATCCCCAATCCCCAATCAGTITTTCTCTTTCTTACTCCTCTCTCTCTTTACCCTC 500 	AAACTCATCAAAAACACTACTCCTCTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 	421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 480 	361 TCTCCAACCAAAACATCAATGATTTAATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 . 	301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360 	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300 	181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240 	121 TTTTCTCTTTACAGGGGAGAAITTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180 	61 TAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATACATTCTATGATCATGCT 120 	1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60 	Query Match     80.8%; Score 1379.2; DB 1; Length 2781;       Best Local Similarity     99.4%; Pred. No. 7.9e-280;       Matches     1384; Conservative     0; Mismatches     8; Indels     0; Gaps     0;	Sequence 2781 BP; 861 A; 531 C; 563 G; 826 T; 0 U; 0 Other;	cloning vehicle may be a modified pAT 153 plasmid. Also claimed is a labelled diagnostic probe comprising a DNA molecule having a single- or double-stranded probe sequence of 15 to 10000 nucleotides long Factor IX DNA sequence. (Updated on 25-MAR-2003 to correct PA field.)	The inventors claim a recombinant DNA having a human factor IX sequence pref. at least 50 nucleotides long, esp. 75-2700 nucleotides. A cloning vector contg. foreign DNA is also claimed. The foreign sequence pref. includes the whole of an exon sequence of the human factor IX genome. The	Example; Fig 9; 49pp; English.	Prodn. of artificial human factor IX - by use of recombinant DNA sequences for host transformation and cultivation.	WPI; 1984-057898/10. P-ESDB; AAP40222.	Brownlee GG, Choo KH;	RES	04-AUG-1982; 82GB-00022486. 16-MAX-1983; 83GB-00012490.	03-AUG-1983; 83GB-00020975.	07-M38-1984

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RESULT 1 ADQ38340 XAC ADQ XAC	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
LT 11 B340 ADQ38340 standard; DNA; 2728 BP.' ADQ38340; 18-NOV-2004 (first entry) Human SNP containing myocardial infarction-associated gene, SEQ ID 3. Human SNP containing myocardial infarction-associated gene, SEQ ID 3. Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds. Homo sapiens.	<ul> <li>6.1 CATEGOTGETTAMAGGAGAGATGGGGGACATTCATTCTCTTATATCTTCTTATATCTTCTTTATACTTCTT</li></ul>
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Qy       1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCCTCTCAC       60         Db       1340 AATGAAAGATGGATTTCCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC       11	<pre>W0200058052-A2. W2 15-JUL-2004. W2 22-DEC-2003; 2003W0-US04097B. W2 22-DEC-2003; 2003W0-US0404 Nucleotide subset of the individual 's individual 's</pre>

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1021       TAATAATTAATGCTTAACAGAAAGAAGAAGAACCGTTCGTT	781       ATATATATATATATATATATATATATATATATATATAT	361 TETECAACCAAAACAT CAATGETTAATTAGETCETTATACAEGATCETTEGETCTAC 420 1700 TETECCAACCAACATCAATGETTAATTAGETCETGETATACAEGAGATCAEGAGATCETTEGETCTAC 1759 421 TETATEACAAGGCCAGTACCACACTCATGAAGAAAGAACAEGAGATGAEGAGGTAGETTACAEGAGGTA 1760 TETATEACAAGGCCAGTACCACACTCATGAAGAAAGAACAEGAGATGAEGTGAEG	41 CANAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGY 
888888888888888888888888888888888888888	888888888888888888888888888888888888888	222 9 9 9 9 6 9 6 9 6 9 6 6 6 6 6 6 6 6	ይ የ <u>አ</u> ይ የአ
27 nucleic acids, where the presence of the SNP is correlated with an 27 altered risk for myocardial infarction in the individual. The invention 27 further comprises: an isolated nucleic acid molecule comprising at least 3 contiguous nucleotides where one of the nucleotides is an SNP given in 27 the specification or its complement and encoding any one of the amino 28 comprising an amino acid equence given in the specification; an isolated polypeptide 29 comprising an amino acid equence given in the specification; an antibody 20 that specifically binds to the polypeptide or its antigen-binding 20 tragment; an amplified polymucleotide containing an SNP given in the 29 specification and which is between about 16 and 1000 nucleotides in 20 nucleic acid molecule; a method of detecting a variant polypeptide; and a 20 nucleic acid molecule; a method of detecting an such in the specification in the invention may be used in gene therapy. The 20 myocardial infarction. The novel detection method has cardiant activity. 20 The nucleic acids of the invention may be used in gene therapy. The 20 method is useful in identifying an individual who has an increased or 20 decreased risk for developing myocardial infarction. This 20 polynucleotide sequence represents a human myocardial infarction. Note: This 21 associated gene containing one or more SNP's of the invention. Note: This	<pre>Cargill M, Devlin JJ, Iakoubova O; WPI; 2004-533949/51. P-PSDB; ADQ39166. Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids. Claim 7; SEQ ID NO 1; 145pp; English. Claim 7; SEQ ID NO 1; 145pp; English. The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method has an altered risk for developing myocardial infarction. The method the nucleotide sequences given in the specification in the individual's</pre>	RESULT 12 ADQ38338 ID ADQ38338; XX AC ADQ38338; XX AC ADQ38338; XX IB-NOV-2004 (first entry) XX Human SNP containing myocardial infarction-associated gene, SEQ ID 1. XX Myocardial infarction; detection; single nucleotide polymorphism; SNP; XX Wyocardiant; gene therapy; human; gene; ds. XX Homo sapiens. XX MW02004058052-A2. XX I5-JUL-2004. I5-JUL-2004. 22-DEC-2003; 2003WO-US040978. XX 22-DEC-2003; 2003WO-US040978. XX 20-DEC-2003; 2003US-0434778P. PR 10-MAR-2003; 2003US-045412P. PR 23-SEP-2003; 2003US-045412P. PR 23-SEP-2003; 2003US-0504955P. XX (APEL-) APPLERA CORP.	<pre>y 1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATT</pre>

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QY       781       ATATATATATATATATATATATATATATATATATATAT	<pre>equence was not shown in the specification. The sequence has come from cc an electronic sequence listing downloaded from the wipo website. Sequence 2771 BF; 600 A; 455 C; 456 G; 753 T; 0 U; 273 Other; Duey Match 1393 (Conservative 13), secre 1376, 6; DB 13); Length 2771, Best Local Similarity 29.08; Pred: No. 2.86-97; Inel: 2, Gaps 1, Hatches 139, Conservative 11, Mismitches 00; Inel: 2, Gaps 1, Hatches 139, Conservative 11, Mismitches 00; Inel: 2, Gaps 1, Hat MCTANCOLTIFICCANCETTIVITIANTICANTINANAUCHICHINANTIALCUSCICIUM 1413 MCTANCOLTIFICCANCETTIVITIANTICANTINANAUCHICHINANTIALCUSCICIUM 1509 112 THTPC/THTPC/CANCETTIVICANCETTICANAUXANAUXAN 1520 112 Characteristics 11, Mismitches 01 1530 Characteristics 11, Mismitches 01 1551 Characteristics 11, Mismitches 01 1552 Characteristics 11, Mismitches 01 1553 Characteristics 11, Mismitches 01 1554 Characteristics 11, Mismitches 01 1555 Characteristics 11, Mismitches 01 1555 Characteristics 11, Mismitches 01 1557 Characteristics 11, Mismitches 01 1558 Characteristics 11, Mismitches 01 1559 11, Mismitches 01 1550 11, Mismitches 01 1551 11, Mis</pre>
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<u> 1,1 = 1111</u>	
	QY       1         DB       2         QY       1         DB       2         QY       1         DB       2         DB <td< td=""></td<>
<pre>Cargill M, Devlin JJ, Takoubova O; WPI; 2004-533949/51. p-PSDB; ADQ39167. Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids. Claim 7; SEQ ID NO 2; 145pp; English. The invention relates to a novel method for identifying an individual who</pre>	<pre>94. ATCALTGTAACTAAAAAAGCTGACATTGACCGAAACATTATTGTACTGTTTCTAAAAAAATAA 102 211 ATCALTGTAACTAAAAAAACGTGACATTGACCGAAACATATTGTACTGTTTCTAATAAAAATAA 200 212 TTAATAATAATTCAAACAGTGACATTGACCGAAACCGTTCGAAACAAAAATTCAAAAAATTCAAAAAGTGAACGGTTCGAAACAAATTCAAACAGTGTTCTCCAAGCCGAAGCAATTCAAACAAGTGTTCCAAGCGTTCGAAGAAGTTCAAACAAGTGTTCCAAGCGTTCGAAGAAGTATTCAAACAAGTGTTCCAATCAAACAAGTGTTCCAATCAAAAAATTCAAAAAAAGTGTTCCAATCAAACAAGTGTTCCAATCAAACAAGTGTTCCA 210 TTAAATTAATTCAAAAAATTCAAAAGTGTTTCCAATCAAGCGAATCAAACAAGTA 221 AGTTCCCAAAGAAAAATTCAAAAGTGTTCCATTCCAATCAACAAAAATTAAAAAAATTCAAAAAAA</pre>

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361 TCTCCCAACCAAAACATCAATGTTTAATTAGTTCTGTACACGTACAGGATCTTTGGTCTAC 420 1749 TCTCCCAACCAAAACATCAATGTTTAATTAGTTCTGTACACGTACAGGATCTTTGGTCTAC 1808 421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAGAACAACAGGAGTAGCTGACAGGCTA 480 1809 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACAACAGGAGTAGCTGACAGGCTA 1868 481 AAACTCATCAAAGGCCAGTACCACACTCATGAAGAACAACAAGAGTAGCTGAAGGCTA 1868 481 AAACTCATCAAAGGCCAGTACCACTCTTTCCTCATGAAGAAACAACAAGGAGTAGCTGAAGGCTA 1868 481 AAACTCATCAAAACACTACTCCTCTTTCCTCATGAAAGAACAACAAGGAGTAGCTGAAGGCTA 1868 541 CAAATCCCAAAACACTACTCCTTTTCTCTTACCCTCTCCCCCTTTTACCTTTTC 540 	TTTTCTCTTTACAGGGAGAATTTCCATATTTTACCTGAGCAAATTGATAGAAATGGAA 	Query Match       80.6%; Score 1376.6; DB 13; Length 2777;         Best Local Similarity       99.8%; Pred. No. 2.8e-279;         Matches 1388; Conservative       1; Mismatches         1       AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC         60       111111111111111111111111111111111111	has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the mucleic acids of the invention may be used in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The mucleic acids of the invention may be used in farction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide gene containing one or more SNP's of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website. Sequence 2777 BP; 801 A; 489 C; 452 G; 754 T; 0 U; 281 Other;
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			·····
RESULT 14 ADQ3811 ID ADQ38 XX ADQ38 XX ADQ38 XX ADQ38 XX ADQ38 XX ADQ38 XX ADQ38 XX ADQ38 VX ADX VX	0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	8.8 8 8 8 <b>8</b>	5
77.14 ADQ38341 standard; DNA; 2831 BP. ADQ38341; 18-NOV-2004 (first entry) Human SNP containing myocardial infarction-associated gene, SEQ ID 4. Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; gene; ds. Homo sapiens. WO2004058052-A2.	1201       GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 	111111111111111111111111111111111111	601       CATGGTCGTTAAAGGAGAGGAGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA         1989       CATGGTCGTTAAAGGAGAGAGATGGGGAGCATCATTCTGTATACTTCTGTACACAGTTATA         661       CATGTCTATCAAACCCAGACTTGCTTGCTTCCATAGTGAGACTTGCTTG

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CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGGCCTTGA 			1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60 	Query Match 80.6%; Score 1376.6; DB 13; Length 2831; Best Local Similarity 99.8%; Pred. No. 2.8e-279; Matches 1388; Conservative 1; Mismatches 0; Indels 2; Gaps 1;		composition for treating of preventing myocardial infarction- polynucleotide sequence represents a human myocardial infarction. associated gene containing one or more SNP's of the invention. Note: This	method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a		specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a	acid sequences given in the specification; an isotated polypeptive comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding	further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino	altered risk for myocardial infarction in the individual. The invention	The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide semiences given in the specification in the individual's	•	Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.	WPI; 2004-533949/51. P-PSDB; ADQ39169.	Cargill M, Devlin JJ, Iakoubova O;	(APPL-) APPLERA CORP.	30-APR-2003; 2003US-0466412P. 33-APR-2003; 2003US-0466412P. 23-SBP-2003; 2003US-0504955P.	20-DBC-2002; 2002US-0434778P.	22-DRC-2003: 2003WO-US040978.	15-JUL-2004.
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Query Match 80.5%; Score 1373.4; DB 13; Length 2758;	2758 BP; 858	invention. Note: The sequence ( ne printed specification, but v	polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polymucleotide of	molecules may also be used in genetic mapping, in identifying individuals from minute biological samples. In deterting single michoride	aucoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp	used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders,	selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diarneric polynucleotide of the invention diarneric formation of the second seco	Claim 1; Page; 190pp; English. The invention relates to novel diagnostic and therapeutic polynucleotides	in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.	WPI; 2004-329368/30. P-PSDB; ABM84453. New diagnostic and therapeutic polynucleotides and polyneptides useful	Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson J S, Shi X, Suarez CJ;	Rioux P, Shen EJ, Wu MC, Si art EA, Wingrove J, Vitt UA	Schmadt JF, Wright NJ, Brung CW, Marjanovic MY, Shen F, Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV; Mooney EM, Delegeane AM, Panegar IS, Banville SC, Reddy TP; Steveng KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;	YTE CORP.	12-SEP-2002; 2002US-0410259P. 12-SEP-2002; 2002US-0410260P.	12-SEP-2003; 2003WO-US028227.	25-MAR-2004.	WO2004023973-A2.	Along sapiens:	B; gene; gene therapy; human diagnostic and therapeutic polynucleotide;	ostic and	18-NOV-2004 (first entry)	ACN43105.			1381 TECERGETECAT 1391                2821 TECERGETECAT 2811	2761 CIICIAGAGAGIIGCIGACCIGACGIAIGIIICCCITIGIGAATTAATAAACIG3TG 2820	
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¥	1081	CTTTGAGGAAGAATTCAACAGTGTGTGTGTGTGAGCAGTGTTCAGAGCCAAGCAAG
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र	1141	AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCCGAAGTG 1200
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R	1201	CAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260
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X	1261	TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320
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505 361	101 385 241 445 301	121 325	205 61	145 1	in Bry Match Br Local Similarity 99.4%; Pred. No. 6e-104; Prede 5792; Conservative 0: Mignatches 3;	2	/db_xref="taxon:9606" /clone="117N670205n1-6-A08" /sex="F" /lab_host="Top10F'" /clone_1ib="L17N670205n1"	rce 1	Pax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 6 row: A ccolumn: 08 High quality sequence stop: 532.			FERENCE AUTHORS	M	4 ON	
<b>ш</b> п	101 385 241 445 301		205 61	145 CATATITTACCTGAGCAAATGATTAGAAAATGGAACCACTAGAGGAATATAATA 	in Bry Match Bry Match St Local Similarity 99.4%; Score 527.2; DB St Local Similarity 99.4%; Score 527.2; DB	<pre>/note="Organ: Diver; Vector: piris-rac; site_i score; Site_2: Not1; The library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."</pre>	/db_xref="taxon:9606" /clone="L17N670205n1-6-A08" /sex="F" /lab_host="Top10F'" /clone_lib="L17N670205n1"	rce 1	Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 6 row: A column: 08 High quality sequence stop: 532.			FERENCE AUTHORS	SM Homo Bukar Mamma	DN K-EST021594( L17N670205nJ V CB156936 CB156936.1 EST.	

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RESULT 3 BX414387/c LOCUS REFERENCE AUTHORS VERSION KEYWORDS Ś 昂 昂 S Ş 昂 Ş 昂 Ş 븅 ą FEATURBS COMMENT SOURCE DEFINITION ORIGIN ACCESSION ORGANISM Matches Query Match Best Local Similarity TITLB JOURNAL BOUTCE 1047 481 625 421 565 395 987 927 867 455 515 INCACACATATAATGGAAGCAATAAGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTG 489; Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; BST This sequence belongs to sequence cluster 10715.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBAK078AH02NM1&c=10715.f. 1 (bases 1 to 515) Li,W.B., Gruber,C., Jessee, Full-length cDNA libraries Unpublished (2001) Homo Homo BX414387.2 GI:46928493 Contact: Genoscope On May 13, 2003 this sequence version replaced gi:30645720 Hominidae; Homo. GAGCATCATTCTGTTATACTTCTGTACACAGGTTATACATGTCTATCAAACCC 676 GAGCATCATTCTGTTATACTTCTGTACACAGTTATACATGTCTATCAAAACCC 532 TACACACATATAATGGAAGCAATAAGCCATTCTAAGAGCCTTGTATGGTTATGGAGGTCTG 926 GAACCGTTCGTTTGCAATCTACAGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGT 1106 ACTAGGCATGATTTCACGAAGGCAAGATTGGCATATCATTGTAACTAAAAAAAGCTGACAT 986 ACTAGGCATGATTTCACGAAGGCAAGATTGGCATATCATTGTAACTAAAAAAAGCTGACAT sapiens sapiens (human) Conservative /clone="CSODMOOSTIOS" /tissue\_type="FETAL LIVER" /dev\_stage="fetal" /clone\_lib="Homo sapiens FETAL LIVER" /note="Organ: liver; Vector: pCMVSPORT\_6; lst strand cDNA was primed with a NotI-oligo (dT) primeT. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized." /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" Location/Qualifiers .515 28.5%; 99.0%; Jessee,J. and Polayes,D. praries and normalization 0 Score 486.6; DB 5; Pred. No. 4.1e-95; 0; Mismatches 5; Indels Length 515; °, Gaps 624 396 336 480 456 0 REFERENCE AUTHORS ACCESSION VERSION KEYWORDS LOCUS DEFINITION RESULT 4 CO775183 Ş 昂 ą 昂 Q Ś 昂 Ş 昂 昂 昂 FEATURES COMMENT SOURCE JOURNAL TITLE ORGANI SM PUBMBD Bource 1347 1107 1287 1227 215 335 155 275 95 ы С ILLUMIGEN MCO 52421 Katze MNLV Macaca nemestrina CDNA clone IBIUW:28456 57 similar to Bases 5 to 424 highly similar to 1 Seq primer: CCCTCACTAAAGGGAACAAAA POLYA=Yes. FORWARD: CCCTCACTAAAGGGAACAAAA BACKWARD: CACTATAGGGCGAATTGGGTA Insert Length: 524 Std Error: Plate: CL000532 row: F column Fax: 2063780408 Email: cmagness@illumigen.com Sequenced on 2004.07.21. 661 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see http://www.macaque.org Indonato, S.P. Analysis of the Macaca mulatta transcriptome divergence between Macaca and human Genome Biol. 6 (7), R60 (2005) 1 (bases 1 to 524) Magness, C.L., Pellin, P.C., Proll, S.C., Fitzgibbon, M., Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Cercopithecidae, Cercopithecinae, Macaca. Macaca nemestrina (pig-tailed macaque) Macaca nemestrina EST (Hs.1330), mRNA sequence. CO775183 Contact: C. Magness CO775183.1 GI:50976446 CO775183 2203 Airport Way S, Suite 450, Tel: 2063780400 PCR PRimers Illumigen Biosciences Inc. 15998449 CTTCAGCAGTGTTCAGAGCCAAGCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGT 1166 ATAAGTCATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAA ATAAGTCATTCCAATCAGCCAACTAAGTTGTCCTTTTTCTGGTTTTCGTGTTCACCATGGAA 1286 ATCATGTCTCCTTTAACTAGCATACCCCGAAGTGGAGAAGGGTGCAGCAGCTCAAAGGC CGTAGTTTCCCTTT CGTAIGITICCCTT 1360 CATTTTGATTATAGITTAATCCTTCTATCTTGAATCTTCTAGAGAGTTGCTGACCAACTGA CTTCAGCAGIGITICAGAGCCAAGCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGT /db\_xref="taxon:9545" ' /clone="IBIUW:28458" /strain="Indian" /organism="Macaca nemestrina" /mol\_type="mRNA" 'clone\_lib="Katze\_MNLV" lab\_host="Electromax DH10B" sex="male" . .524 ocation/Qualifiers 22 Std Error: 0 v: F column: ( column: 524 bp Thomas, M.J., Korth, M.J., Agy, M.B., Scherer, C.A., Miner, D.G., Katze, M.G. Seattle, 0<u>7</u> 8 mRINA WA 98134, linear and the sequence USA BST 04-AUG-2004 human F9 156 216 276 36 96 and

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	TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) PHEMED 10449764	ae; Homo. ae; Homo. es 1 to 518) s,G.G., Wallace,J.C., Smith,K., A., Shaker,R., Furlong,J., Youn	SOURCE Homo sapiens (human) ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Butheria: Euarchontocilizes: Primazes: Catarzhini	genomic clone Plate=742 Col=19 Rów=B, genomic survey se 1 AQ456663 AQ456663.1 GI:4591998 ASS.	518 bp DNJ T7A RPCI-11 Human Male	485 AGGACTACTGACAAAATCACTTCGACCCCGCCAAGCTGCT	1452 GGGACTACTAGGAAAAATGACTGTGACGGGGAAGGGGGT 1491			0Y       1212       AGAMGEC MANAGEMENT (ALL MARKINAGET (CLITTE (27))         Db       245       AGCAGGETCGAAGACATAAGTCATTCCAATCAGECAAGTAGTTGTCCTTTTTCTGGTTTC 304         0Y       1272       GTGTTCACCATGGAAGACATTAGAGTCAATTCCAATCAGECTAAGTTGTATCTTTGTAATCTTCTGGTTTC 304	1153 CAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCC-GAAGTGGAGAAGGGTGC 185 [1]	Qy         1093         ATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	Qy         1033         TAACAGAAAGAGAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGACTTTGAGGAAGA         1092	Qy         974         алаладствасаттерасссадасататтерастеттесталала-таатлатаатаатдае 1032         1111<	Query Match 26.4%; Score 451.2; DB 7; Length 524; Best Local Similarity 94.2%; Pred. No. 2.1e-87; Matches 490; Conservative 0; Mismatches 28; Indels 2; Gaps 2;	<pre>/note="Organ: liver; Vector: pDONR 222; Site 1: BsrG I; Site_2: BsrG I; Created from CloneMiner cDNA Library Construction kit (catalog #18249-029)"</pre>
<ul> <li>RESULT 6 AV647038</li> <li>LOCUS AV647038</li> <li>JOSEFINITION AV647038 GLC Homo sapiens cDNA clone GLCAUA09 3', mRNA sequence.</li> <li>ACCESSION AV647038.1 GI:9868052</li> </ul>	Qy 1571 TGTC 1574 Db 515 TGTC 518	1511 455	QY         1451         TGGGACTACTGACAAAATCACTCTGACCCCTGCCAAGCTGCTGCCCTTCTCCTGCCCCAACC         1510           Db         395         TGGGACTACTGACAAAATCACTCTGACCCCGCCAAGCTGCCTTCTCCCTGCCCCAACC         454	QY         1391         TACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATTTGATGATGCA         1450           Db         335         TACCTTGGCTTTTTGTGGATTCCATTGATGTGAATCACTCAC	QY       1331       GTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTGTTCTGGTTCA       1390	Oy         1271         CGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAGAGA         1330           Db         215         CGTGTTCACCATGGAACATTTTGATTATAGNTAATCCTTCTATCTTGAATCTTCTAGAGA         274	Oy         1211         CAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTT         1270           Db	Qy         1151         ACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTGGAGAAAGGGTG         1210           Db         95         ACCAGATGACATTTTTATCATGTCTCCTTTAACTAGCATACCCCGAAGTGGAGAAAGGTG         154	QY       1091       GAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	Query Match 26.1%; Score 446; DB 9; Length 518; Best Local Similarity 94.6%; Pred. No. 2.8e-86; Matches 458; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" ORIGIN	/sex="male" /clone_lib="RPCI-11 Human Male BAC Library" /note="Vector: pBACe3.6; Site_1: BcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor	(신희) (신희) (신희)	Class: BAC ends Class: BAC ends High quality sequence stop: 518. FEATURES Location/Qualifiers	or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 742 row: B column: 19 Ser 742 roy: B column: 19	Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from

RESULT 7 Av647182	5 5 5	A A A	8 Q	88	5 Q	р <b>2</b> 2	, <b>6</b>	Query Mat Best Loca Matches	ORIGIN			0044	FEATURES			JOURNAL PUBMED COMMENT	TITLE	·	REFERENCE AUTHORS	-	KEYWORDS SOURCE ORGANISM	
	478 CTAAAACTCATCA 490                361 CTAAAACTCATCA 373	418         TACTCTATCACAAGACCACGAGTACCACCACTCATGAAGAAGAACACAGGAGTAGCTGAGAGG         477	358 GCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTC 417 	298 TGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTT 357 	238 TGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTA 297 	178         GAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCT         237	118 GCTTITITCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGATAGA	Query Match 21.9%; Score 373; DB 1; Length 373; Best Local Similarity 100.0%; Pred. No. 2.2e-70; Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	/GD/GD/GD/GD/GD/GD/GD/GD/GD/GD/GD/GD/GD/	/org /mol		Tel: 86-21-50801919(ex.45) Pax: 86-21-50801922 Email: hanzg@chgc.sh.cn	Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203. P. R. China	proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) 11752456 Contact: Zequang Han	Insight into hepatocellular carcinggenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver	Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,V., nu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.	1 (bases 1 to 373) Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,	Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini; Hominidae, Homo.	BST. Homo sapiens (human) Homo sapiens	
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ы 4 А	у да	р В б	5 8 8	&	1 20 20	QY 40	Query Match Best Local   Matches 37	ORIGIN			Bource	FEATURES		COMMENT	JOURNAL PUBMED	TITLS	AUTHORS	REFERENCE	ORGANISM	VERSION KEYWORDS SOURCE	LOCUS DEFINITION ACCESSION	
478 CTAAAACTCATCA 490                 361 CTAAAACTCATCA 373	418         TACTCTATCACAAGGCCAGTACCACACCACACTAAGAAGAACAAGACAGGAGTAGCTGAGAGG         477	358         GCTTCTCCAACCAAAACATCATGTTTATTAGTTCTGTATACAGTACGATCTTGGTC         417			178         GAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCT         237		21.9%; Score 373; DB 1; Length 374; Similarity 100.0%; Pred. No. 2.2e-70; 3; Conservative 0; Mismatches 0; Indels 0; Gaps	<pre>/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:</pre>		/mdl_type="mtxA4" /db_xref="taxon:9606" /clone="tlcAVP01"		Email: hanzgechgc.sh.cn This clone is available at CHGC in Shanghai. Location/Qualifiers	201203, F. K. CHING Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai	with those of corresponding noncancerous inver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) 11752456	H1,G2, G1,J2, Chen,Z, and H41,Z. Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma	Xu,X., Huang,U., Au,Z., QLau,P., Ant,Z., Li,N., Du,J., Hu,Y., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,Y., Shen,K., Lu,G., Pu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,	Hominidae, Homo. Hominidae, Homo. 1 (bases 1 to 374) 1 (bases 1 to 374)	HOMO SADDENS METAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchoncoglires; Primates; Catarrhini;	AV64 EST. Homo	AV647182 AV647182 GLC AV647182	

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Qy       993       AGACATATTGTACTCTTTCTAAAAATAATAATAATAATGCTAACAGAAAGAA	us liver 1: Bcori 1: Bcori 1: Bcori 385; 54; 6CTGACAT GCTGACAT	REFERENCE 1 (bases 1 to 385) AUTHORS X1, X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z. TITLE Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001) 11752456 COMMENT Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai	SULT 8 656454 CUS 5 PINITION CESSION RSION RSION RSION RSION RCB URCB URCB
Db       569       CTMAATAATCACTTTCCCTTTCAAGGGTAATTTCC       512         QY       120       FTFTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTTCC       512         Db       511       FTTTTTTTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGAT       169         QY       170       AGAAAATGGAACCACCTAGAGGAAATTTAAGGAACTTCATTTTTTTCTAGAAATAAGTAGATA       452         QY       170       AGAAAATGGAACCACCTAGAGGAAATTAAGTGTGTTAGGAAATTACAGTCATTTTTTTCTAAGTAAG	JOURNAL       Unpublished (2005)       contact: Anderson SI         Genomics and Bioinformatics       Roslin Institute         Roslin Institute       I721         Bource       /organism="Bos taurus"         /mol type="mtxbus"       //dissue type="mtxbus"         /mol type="mtxbus"       //clone_lib="fiver"         /clone_lib="KN-252-liver"       Bos taurus"         /mol type="mtxbus"       //note="fiver"         /clone_lib="KN-252-liver"       Bos taurus"         /clone_lib="KN-252-liver"       Bos taurus"         /note="breed: N'dama"       /note="breed: N'dama"         ORIGIN       13.9%; Score 236.8; DB 1; Length 721;         Best Local Similarity 67.9%; Pred. No. 9.6e-41;       Matches 429; Conservative 0; Mismatches 177; Indels 26; Gaps 6;         QY       1 AATGAAAAATGAATGAATTGAATTGAATTGAAATTGAAAGGCCCTTTA 570         Db       629 AAAGAAAAATGAATGAATTTTTTTTTTTGAAATTAATATATATGAACATGGACAAGGTCCTTTA 570         QY       60 CTAATCTATTCCAATCATTTTTTTTTTGAAATTATATATA	3', mRNA AM018125 AM018125 EST. Bos taurr Mammalia Pecora; E Pecora; E 1 (basec 1 (basec 1 (basec 1 (basec) 1 (basec)	

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No. 8.1e-25 matches 13 ATTTCACGAAC	y Match9.6%; Score 163.6; I	<pre>/note="Vector: prripi8x2; site_1: sfil GGCCATTACGGCC; /note="Vector: prripi8x2; site_1: sfil GGCCATTACGGCC; site_2: sfil GGCCGCCTCGGCC; Normalized cDNA library prepared from liver of hibernating and summer animals"</pre>	/sex="Male & female" /tissue_type="liver" /dev stage="Adult" /lab host="E.coli Electromax DH10B" /lab host="E.coli Electromax DH10B"	/organism="Spermophilus lateralis" /mol_type="mRNA" /db_xref="texcon:76772" /clone="27j01"	Plate: 27 row: J Columni: 05 of COCGGAAGCGCGCCATTGTGTTGGT-3') Seq primer: TriplEx 5'LD (5'-CTCGGGAAGCGCGCCATTGTGTTGGT-3') High quality sequence stop: 583 PEATURES Location/Qualifiers source 1583	Tel: +44(0)151-795-4510 Fax: +44(0)151-795-4431 Email: cossingaliv.ac.uk Vector has been trimmed from this EST.	Laboratory for Environmental Gene Regulation University of Liverpool School of Biological Sciences, The Biosciences Building, Crown Street, Liverpool, United Kingdom, L69 72B	quirrel,	REFERENCE 1 (bases 1 to 583) AUTHORS Williams,D.R., Gracey,A.Y., Martin,S.L., Hughes,M.A., Li,W., Rogers,J. and Cossins,A.R.	ORGANISM Spermophilus lateralis Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Sciuridae; Xerinae; Marmotini; Spermophilus.	CO740602 CO740602.1 C EST. Spermophilus	CO740602 LOCUS CO740602 583 bp mRNA linear EST 29-JUL-2004 DEFINITION SILL07a27j01f1 squirrel liver library 3 Spermophilus lateralis cDNA clone 27j01 5', mRNA sequence.	Db 43 TACATAGGCALTAAAGGGGGGAAAAGGAGGAAAAAGAAAAAAAAAA	CCTTTTACCCTCCATGGTCGTTAAAGGAGAGA 620	529 TITTACCTITICCAAATCCCAAATCAGTTITTCTCTTTCTTACTCCCCTCTCT	470	Db 276 TTTTTTTAACATCCCCCCCAAGTTAAAATTTATTGGATTGTATCCAGGAT 224 Oy 410 CTTTGGTCTACTCTCACAAGGCCAGTACCACGACTCATGAAAGAACACAGGAGTAG 469 U
ORIGIN /clone_lib="Pig liver cDNA" ORIGIN Query Match 8.8%; Score 149.6; DB 6; Length 374;	/mol_type="mttNA" /db_xref="taxon:9823" /clone="04D3"	. FEATURES FOLYA=Yes. BOUTCE Location/Qualifiers 1. 374 /organism="Sus scrofa"	PCK PKIMETS PORWARD: ACAATTTCACACAGGAGCTAGCAGAC BACKWARD: ACGACTCACTATAGGGCTTTTTTTTTTTTTTAC Insert Length: 374 Std Brior: 0.00 Seq primer: M13P	11 10081	JOURNAL Unpublished (2003) COMMENT Contact: Ernst CW Animal Science Molecular Genetics Lab Michigan State University	AUTHORS Ernst, C.W., Raney, N.B., Martinez, M.M., Hargrave, K.M., Hill, G.M. and Link, J.B. TITLB Identification of differentially expressed genes in pig liver	' Sue Sue	5	(TION ZP0904D3 Pig liver cDNA Sus scrofa cDNA clone 04D3 simil Coagulation Factor IX (F9), mRNA sequence.	RESULT 11 CF106639 CF106639 374 bp mRNA linear EST 22-JUL-2003	$ \begin{array}{cccc} Qy & 1330 \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ $	DY 1270 TCGTGTTCACCATGGAACATTTGATTATAGTTAATCCTTCTATCTTGAATCTTCTAAG 1329 		Db 340 ACCAGAAGACATAAGTATCATGTCTCCTTTAACTAGCATACCAGAGTGGAGAAGGACA 396		DY 1031 GCTAACAGAAAGAAGAAGAGACGITUGUTUGUAUUUAGAGUAAGAAGAGAGATUGUAGAGUA 	Db 120 TGATTATGGCAGTCTGGCTGGGAATGGTTCCATCAAGGCAAGGCTGCAGGTCACTAA 176 QY 971 CTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAAATAATAATAATAATAATAAT 

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ORIGIN ACCESSION VERSION RESULT 12 EX926315 FEATURES COMMENT SOURCE REFERENCE KBYWORDS DEFINITION Query Match TITLE AUTHORS JOURNAL ORGANISM Matches Best Bource Local Similarity 75.4 hes 226; Conservative 260 665 140 721 200 CCTATCAAACCCAGTCTTGCTTTCAATTTGTTCTTGGACTTGCTGTTCATAGCACAGGGA 605 545 486 80 20 Sequence cleaned of vector, adaptator and at sigenasupport@jouy.inra.fr to obtain th cedex, FRANCE Institut National de la Recherche Agronomique Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan Bonnet;A., Tosser-Klopp,G., Be Soares,M., Bonaldo,F. and Hate A Pig Normalised Multi-Tissue Unpublished (2003) Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08 Genetique Animale Contact: Tosser-Klopp G 8ns BX926315 688 bp mRNA BX926315 Sus Scrofa library (scan) Sus scan0021d.c.01 5prim, mRNA sequence. Plate: Bukaryota; Metazoa; Mammalia; Butheria; Sus scrofa BST scan0021d.c.01 5prim, BX926315 sequence Email: tosser@toulouse.inra.fr Sus scrofa (pig) BX926315.1 TGAAGTAAGGTGCCTGAA---CTTGGAGGAAAAGTTCCTCTTGGAGAGTCACATTATT 314 TCTATCAAACCCAGACTTGCTTCCATAGTG----GAGACTTGCTTTTCAGAACATAGGGA 720 GGCATTAAAGGAGGGAAGGGGAGCATCATACTGTTTTACTGCTGTACACAATGATGCAAA 199 GTCGTTAAAGGAGAGAGGAGGAGGAGGATCATCTGTTATACTTCTGTACACAGTTATACATG 664 TCCCAATCCCCAAATCAGITTTTCTCTTTCTTACTCCCTCTCCCCTTTTACCCCTCCAIG CATCATAAACGCIGCAICITTCICCGIACCCTIGGICCIGCAICIGCTAICITTCCCAAC CATCAAAAACACTACTCCTTTTCCTCTACCC-TATTCCTCAATCTTTTACCTTTTCCAAA (bases 1 to 688) 0021 row; c column: 1. Location/Qualifiers /organism="Sus scrofa" /mol type="mRNA" /db xrefe"taxon:9823" /clone="scan0021d.c.01" /tissue\_type="mixed" /dev\_stage="from embryos to adults" /clone lib="Sus Scrofa library (scan)" /note="tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, panoreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epiddymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder" Tosser-Klopp,G., Benne,F., Bonaldo,F. and Hatey,F. GI:41143163 . 688 75.8%; 8.8%; Chordata; Craniata; Vertebrata; Euteleostomi; Laurasiatheria; Cetartiodactyla; Suina; Suida <u>;</u> Score 149.6; Pred. No. 8.9e-22; 0; Mismatches 64 **cDNA** Library mRNA 멻 Cabau, C., 64; . .. scrofa the repetitions. Length 688; linear Indels chromatogram CDNA Villeger,S., clone EST 07-MAY-2004 8; Contact us am of this Gape Suidae; 778 139 544 259 604 79 3 ACCESSION VERSION KEYWORDS RESULT 13 BX925779 ORIGIN FEATURES Ś 昂 Ş Ş COMMENT REFERENCE SOURCE DEFINITION LOCUS 昂 뭉 昂 Ś 昂 Q Query Match TITLE JOURNAL AUTHORS ORGANISM Matches Best Local Similarity source 261 201 141 605 721 665 TCTATCAAACCCAGACTTGCTTCCATAGTG----GAGACTTGCTTTTCAGAACATAGGGA 720 545 ICCCAAICCCCAAAICAGITITICICITICITACICCCTCICCCTTITACCCCICCAIG 604 486 81 21 226; Institut National de la Recherche Chemin de Borde-Rouge - Auzeville cedex, FRANCE Sus scrofa (pig) Sus scrofa Plate: 0021 sequence Sequence cleaned of vector, adaptator and r at sigenasupport@jouy.inra.fr to obtain the Tel: 33 (0) 5.61.28.51.14 Fax: 33 (0) 5.61.28.53.08 A Pig Normalised Multi-Tissue Unpublished (2003) Bonnet,A., Tosser-Klopp,G., Benne,F., Soares,M., Bonaldo,F. and Hatey,F. BST scan0021d.o.01 5prim, BX925779 BX925779 Sus Scrofa library (scan) Genetique Animale Contact: Tosser-Klopp G BUS Eukaryota; Metazoa; Mammalia; Eutheria; BX925779.1 Email: tosser@toulouse.inra.fr CCTATCAAACCCAGTCTTGCTTTCAATTTGTTCTTGGACTTGCTGTTCATAGCACTGGGA CATCAAAAAACACTACTCCTTTTCCTCTACCC-TATTCCTCAATCTTTTACCTTTTCCAAAA 544 TGAAGTAAGGTGCCTGAA---CTTGGAGGAAAAGTTCCTCTTGGAGAGTCACATTATT 315 GTCGTTAAAGGAGAGAGGGGGGGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATACATG CATCAGAAACGCTGCATCTTTCTCGGTACCCTTGGTCCTGCATCTGCTATCTTTTCCAAC (bases 1 to 690) GGCATTIAÀ À GGÀGGGÀ À GGGÀGCÀTCATA CTGTTTTÀ CTGCTGTÀ CA CA ATGÀTGCÀAA Conservative /dev stage="from embryos to adults" /clome lib="Sus Scrofa library (scan)" /notes="tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, haart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder" /mol\_type="mRNA" /db\_xref="taxon:9823" /clone="scan0021d.o.01" /tlssue\_type="mixed" 21 row: o column: 1. Location/Qualifiers organism="Sus scrofa" .690 GI:41142627 8.8%; 75.8%; Chordata; Craniata; Vertebrata; Buteleostomi; Laurasiatheria; Cetartiodactyla; Suina; Suida °, Score mRNA Pred. No. 9.1e ); Mismatches sequence. 149.6; CDNA 9.1e-22; ches 64; Agronomique BP27, 31326 Castanet-Tolosan Sug Library mRINA B Cabau, C., ς ... A linear scrofa cDNA repetitions. Length Indels chromatogram Villeger,S., ; 069 clone EST 07-MAY-2004 8; Contact am of thi Gaps uretral act us this Suidae; 260 200 .140 664 80 ω

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FEATURES Source	JOURNAL PUBMED COMMENT COMMENT	REFERENCE AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	SULT 14 775581 CUS FINITION	5 8 8 8	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	Best Loc Matches
	Genome Biol. 6 (7), R60 (2005) 15998449 Contact: C. Magness Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400 Fax: 2063780408 Email: cmagnessGallumigen.com Sequenced on 2004.07.29. 411 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see http://www.macaque.org	(bases 1 to 257) 1 (bases 1 to 257) Magness,C.L., Fellin, P.C., Thomas,M.J., Korth,M.J., Agy,M.B., Proll,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and Iadonato,S.P. Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human	ta; Euteleostomi; Catarrhini;	AUNY STATE OF A STATE	665 TCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720 		al Similarity 75.8%; Pred. No. 9.1e-22; 226; Conservative 0; Mismatches 64; Indels 8; Gaps 3;
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Y Match Local ( 1221 388 1281 1281 328 328 328	FEATURES Source ORIGIN	AL	MS R S	T 15 325/c ITION ITION SION SION ON RDS	63 737 123	y Match Local s hes 15: 617 3	ORIGIN
ch       8.3%;       Score 142.4;       DB 7;       Length 400;         1 Similarity       67.9%;       Pred. No. 3.3e-20;       Indels 22;       Gaps 2;         239;       Conservative       0;       Mismatches 91;       Indels 22;       Gaps 2;         21 AAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCTTTTCTGGTTTCCGGTTTCGGTTTCACC 1280         1		Unpublished (2004) Contact: Thomas Schlueter LION bioscience AG Waldhoferstrasse 98, D-69123 Heidelberg, Germany Tel: +49 6221 4038 150 Fax: +49 6221 4038 290 Fax: +49 6221 4038 290	Canis familiaris (dog) Canis familiaris (dog) Canis familiaris Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Butheria; Laurasiatheria; Carnivora; Pissipedia; Canidas; Canis. Canis. 1 (bases 1 to 400) 1 (bases 1 to 400) Schlueter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H., Schlueter,J. and Loebbert,R. Henrich,J. and Loebbert,R.	CO701325 DG32-1f6 DG32-liver Canis familiaris cDNA 3', mRNA sequence. CO701325.1 GI:50649993 BST.		h B.6%; Score 147; DB 7; Length 257; .Similarity 93.9%; Pred. No. 3.3e-21; .53; Conservative 0; Mismatches 10; Indels 0; Gaps 0 	<pre>/note="Organ: liver; Vector: pDONR 222; Site_1: BarG I; "Site_2: BarG I; Created from CloneMiner cDNA Library Construction kit (catalog #18249-029)"</pre>

뭥 昂 Ş Search completed: April 18, 2006, 15:20:39 Job time : 8293.18 secs 뭥 Ş ą Mon Apr 24 07:43:09 2006 1441 TGATGATGGATGGGACTACTGACAAAATCA--CTCTGACCCTGCCAAGCTGCCTGCCTTCT 1498 148 TTGTTATATATGAGACTACTGACAAAATCATGTTTGGGACCACTTTGACCTGACCAAGCT 89 5 us-09-884-901a-7.rst

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1         11701.8         99.7         38059         3         US-09-328-925-4         Sequence 4, Appli           2         1698.6         99.5         36755         3         US-09-928-925-4         Sequence 16994, A           3         1391         81.5         2775         3         US-09-928-925-4         Sequence 2.2, Appl           4         1391         81.5         2772         3         US-09-928-914-016-5252         Sequence 2.2, Appl           7         1385.8         81.2         2002         3         US-09-928-925-3         Sequence 1. Appl           1         1271.4         74.5         1272         3         US-09-328-925-76         Sequence 3, Appl           11         1271.4         74.5         1273         3         US-09-328-925-76         Sequence 77, Appl           12         1269.8         74.4         1273         3         US-09-328-925-77         Sequence 77, Appl           14         1261         73.9         1272         3         US-09-328-925-79         Sequence 78, Appl           15         1266         73.4         1276         3         US-09-328-925-79         Sequence 78, Appl           16         9.4         1610         2	Result Query No. Score Match Length DB ID Description	1sting ssued_ /cgn /cgn /cgn /cgn /cgn /cgn /cgn the n the n the n	um Match 0% um Match 100	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	mber of hits satisfying chosen paramete	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Cearched. 1101057 gers. 888780828 residues	Title: US-09-884-901A-7 Perfect score: 1707 Sequence: 1 aatgaaagatggatttccaaggagtttcaggccaagctta 1707	Run on: April 18, 2006, 12:23:43 ; Search time 364.148 Seconds (without alignments) 8332.600 Million cell updates/sec	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. OM nucleic - nucleic search, using sw model
1       AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAAACAGGGCCTCTCAC       6         1       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Query Match 99.7%; Score 1701.8; DB 3; Length 38059; Best Local Similarity 99.9%; Pred. No. 0; Matches 1703: Conservative 0; Mismatches 2; Indels 0; Gaps 0;	<pre>10 June 4, Application US/09328925 ree 4, Application US/09328925 L No. 6610906 L INFORMATION: L INFORMATION: Nucleotide sequences for Gene Regulation GANT: Kurachi, Sumiko 3 OF INVENTION: Nucleotide sequences for Gene Regulation 3 OF INVENTION: Sequences for Gene Regulation 3 OF INVENTION UNVENTION: Sequences for Gene Regulation 3 OF INVENTION UNVENTION: Sequences for Gene Regulation 3 OF INVENTION UNVENTION UNVENTION: Sequences for Gene Regulation 3 OF INVENTION UNVENTION: Sequences for Gene Regulation 3 OF INVENTION UNVENTION UNVENTION: Sequences for Gene Regulation 3 OF INVENTION UNVENTION UNVENTION UNVENTION UNVENTION UNVENTION UNVENTION 3 ON 4 OF SEQ ID NOS: 84 3 ON 4 OF Sequences for Gene Regulation 3 ON 4 OF Sequences for Gene Regulation 3</pre>		ALIGNMENTS	81.8 4.8 160018 3 US-09-949-016-12017 sequence 12017 81.8 4.8 160018 3 US-09-949-016-15994 Sequence 15994,	40         82.8         4.9         148783         3         US-09-949-016-12729         sequence         12729           41         82         4.8         21017         3         US-09-949-016-12965         Sequence         12929           42         82         4.8         25118         3         US-09-949-016-12965         Sequence         12928           43         82         4.8         95318         3         US-09-949-016-13998         Sequence         13938           43         82         4.8         95318         3         US-09-949-016-13998         Sequence         13938	6 83 4.9 129327 3 US-09-949-016-12257 7 83 4.9 129327 3 US-09-949-016-15368 8 82.8 4.9 61913 3 US-09-949-016-15338 9 82.8 4.9 61922 3 US-09-949-016-11772	2         B3.4         4.9         B829         3. US-09-949-016-11895         Sequence         14171         Sequence         13723         Sequence         137234         Sequence         137244 <td>3         US-09-328-925-58         Sequence           3         US-09-949-016-16093         Sequence           3         US-09-949-016-155435         Sequence           3         US-09-949-016-160372         Sequence           3         US-09-949-016-162372         Sequence           3         US-09-949-016-152347         Sequence           3         US-09-949-016-15347         Sequence           3         US-09-949-016-17315         Sequence</td>	3         US-09-328-925-58         Sequence           3         US-09-949-016-16093         Sequence           3         US-09-949-016-155435         Sequence           3         US-09-949-016-160372         Sequence           3         US-09-949-016-162372         Sequence           3         US-09-949-016-152347         Sequence           3         US-09-949-016-15347         Sequence           3         US-09-949-016-17315         Sequence

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22 10	r 9	Db	оу рв	QY QY	Q7 D5	Qy J	Best Loc Matches Qy	; ORGANI US-09-053- Query Ma	; SOFTWAR ; SEQ ID N ; LENGTH ; TYPE:	; FILE RE ; CURRENT ; CURRENT ; NUMBER	; APPLICA ; APPLICA ; TITLE O ; TITLE O	; GENERAL ; APPLICA ; APPLICA ; APPLICA	RESULT 3 US-09-053- ; Sequence ; Patent N	Db 35	ФВ 34	рь 34 Qy 34	QY 34	рь 34 Оу . 34

ICANT: Solomon, Robert A. ICANT: Schmidt, Ann Marie OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING OF INVENTION: STROKE OUTCOME REFERENCE: 51917-B NT APPLICATION NUMBER: US/09/053,871A NT FILING DATE: 1998-04-01 NT FILING DATE: 1998-04-01 R OF SEQ ID NOS: 22 ARE: Pate NO 22 TH: 2775 L INFORMATION: CANT: Pinsky, David J. CANT: Stern, David CANT: Rose, Bric Match 81.5%; Score 1391; DB 3; Length 2775; Scal Similarity 100.0%; Pred. No. 0; 3 1391; Conservative 0; Mismatches 0; Indels 0; : DNA NISM: Homo Sapien 3-871A-22 CANT: 1621 34864 1685 1625 1565 -871A-22 e 22, Application US/09053871A No. 6315995 5044 GAGGTTAGGAGTTTCAGGCCAGCCT 35068 1681 GAGGTTAGGAGTTTCAGGCCAAGCT 1705 14984 GCCCAGTGGCTCACGCCTATAATCCCCAGCACTTCTGGAGGCCCAAGGTGGGCGGATCACCT 35043 1501 1505 1445 TAACTAATCACTTTCCCCATCTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 1504 1385 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAAATTGAAAATTAACAGGGCCTCTCAC 1444 301 241 181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240 121 TTTTCTCTTTACAGGGGAGAATTCATATTCATATTTACCTGAGCAAATTGATTAGAAAATGGAA 180 361 61 TAACTAATCACTTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120 1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAAATTGAAAAATTAACAGGGCCCTCTCAC CAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG IGCCCCAACCICACCCCCAGCCAGGCCICACICIIIGCIAGIICCITIAGIICTITIAGIC 34923 TCTCCAACCAAAACATCAATGTTTAATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCCATCTTCCCCGATCTTCTTTGCT 1744 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCCAGCCCTTGA TTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAAATGGAA 1564 PatentIn Ver. GCCCAGTGGCTCACGCCTATAATCCCCAGCACTTCTGGAGGCCAAGGTGGGCGGATCACCT 1680 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTCCTTTAGTC 1560 2.1 0 ;; Gaps 1624 1684 60 <u>,</u>

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Oy         661         CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCAGAACATAGGGA         720           Db         2074         [	Db 2014 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 2073	Db 1954 CAAATCCCAATCCCCAAATCAGTTTTTCTTTTCTTACTCCCTCTCTCT	541 CAAATCCCCAATCCCCAAATCAGTTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCC	OY       481       AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC       540         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 1834 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACAGGAGTAGCTGAGAGGCTA 1893	1774	Db 1714 CAACTAACTCAACTCAACTTTTTCCCTCCTTAGCAGCATCCATC	QY 301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 360	Qy         241         CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG         300	Db 1594 CCACTAGAGGAATATAAATGTGTTAGGAAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 1653	Db 1534 TITTCTCTTTACAGGGGAGAATTTCATATTTTACCTCAGGCAAATTGATTAGAAAATGGAA 1593 Oy 181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240	OY 121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180	Db 1474 TAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATAACATTCTATGATCATTGCT 120			tch al Similarity 100.0%; Pr	ヘマダ	SEQ ID NO 2 LENGTH: 2804	L H	INVENTION: with vehicle vector Arexerce: 6627-FA1170 Application NUMBER: US/10/133,907 FILING DATE: 2002-04-25	; GENERAL INFORMATION: ; APPLICANT: Chien, Kenneth R ; APPLICANT: Hoshijima, Masahiko ; TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Pactor VI	US-10-133-907-2 ; Sequence 2, Application US/10133907 ; Patent No. 6677369

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RESULT 5 US-09-949-016-5252 Sequence 5222, Application US/09949016 Patent No. 6612339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: US/09/949,016 URRENT FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/231,768 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/231,768 PRIOR FILING DATE: 2000-10-00 SEROIR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-00-01 SEQ ID NO 52: 207012 SOFTWARE PastSEQ for Windows VerBion 4.0 SOFTWARE PastSEQ for Windows VerBion 4.0 SOFTWARE HUMAN US-09-949-016-5252	97       711       FRANCETANCECTICSIAAAAGTTIGGGGGAAAAGTTIGGGGGAAAAGTTIGGGGGGGG	
QY       661       CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCAGAACATAGGA       720         Db       2103       CATGTCTATCAAACCCAGACTTGCTTCCGTAGTGGAGACTTGCTTTCAGAACATAGGA       2162         QY       721       TCAAGTAAGGTGCCTGAAACTTGCGTGCGGAAACATTGCGAGAGTTAAGTTATTT       780         Db       2163       TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAAGTTTCTTCAGAAGAGTTAAGTTATTT       222         QY       781       ATATATATATATATATATATATATATATATATATATAT	2 6 2 6 1 5 1 4 1 4 1 3 1 3 1 2 1 1 1 1 5 1 5 1 5 1 5 1 5 1 5 1 5 1	-

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DD 1522 ITTICICITITACAGGGGAGAATTICATATTITACCIGAGCAAATTGATTAGAAAATGGAA 1581 <	121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA	Oy       61 TAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATAACATTCTATGATCATGGT 120         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGCCCTCTCAC 60 	Query Match 81.3%; Score 1387.8; DB 3; Length 2792; Best Local Similarity 99.9%; Pred. No. 0; Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			SOFTWARE: Patentin Ver SEQ ID NO 1 LENGTH: 2792 TYPR. DNA	CURRENT FILING DATE: 1998-07 EARLIER APPLICATION NUMBER: EARLIER FILING DATE: 1997-07 NUMBER OF SEO ID NOS: 2	ITITLE OF INVENTION: Factor IX Antihemophilic Factor with Increased Clotting TITLE OF INVENTION: Activity FILE REFERENCE: 5470-183 CURRENT APPLICATION NUMBER: US/09/118.748A	Patent No. 6531298 GENERAL INFORMATION: APPLICANT: Stafford, Da APPLICANT: Chang. JinLi	ភូមិ	Qy         1381 TTCTGGTTCAT 1391           Db         2823 TTCTGGTTCAT 2833	Qy         1321         CTTCTAGAGAGTTGCTGACCTAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG         1380           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         1261         TTTCTGGTTTCGTGTTCACCATGGAACATTTGATTATAGTTAATCCTTCTATCTTGAAT         1320           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         1201         Gagaagggtgcagcaggctcaaaggcataagtcattccaatcagccaactaagtigtcct         1260	Oy         1141         AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG         1200	Qy         1081         CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	Qy         1021         TAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA         1080           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Q	<u>ନ</u> ସ	D QY	да УУ	Qу Db	Db	QY du	DP AQ	D QY	DP QY	da Ag	ду	da Að	DP - QA	DP QA	DB QY	р S	P Q	Å å
1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT	1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 	1141 AGTTGCCTAGACCAGAGGACATAAGTAYCATGTCTCCTTTAACTAACATACCCCGAAGTG 		1021 TAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 	961 ATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 	901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGÀTTTCACGAAGGCAAGATTGGCAT 	841 TATGCGTGTGTGTAGACACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 	781 ATATATATAATAATATATAAAAATATATAATATAAAAATAATAAAA	721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 	601 CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA 	541 CAAATCCCCAATCCCCAAATCAGTTTTTCTTTTCTTACTCCCTCTCCCCCTTTTACCCTC 	481 AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 	421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 	361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 	301 CAACTAACTCAACTCTCATTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT 	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 	181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 

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; FEATURE: ; NAME/KEY: ; LOCATION: US-08-742-877-1 FILING UALS. FILING UALS. PRICA APPLICATION 1435 PRICA APPLICATION DATA: APPLICATION NUMBER: GB 9408717.8 PILING DATE: 03-MAX-1994 ATTORNEY/AGENT INFORMATION: NAME: FLESHNER, RAZ E. REGISTRATION NUMBER: 34,331 REFERENCE/DOCKET NUMBER: 0623.047) TELECOMMUNICATION NUMBER: 0623.047) TELECOMMUNICATION NUMBER: 0623.047) TELECOMMUNICATION NUMBER: 0623.047) TELECOMMUNICATION NUMBER: 0623.047) RESULT 7 US-08-742-877-1 昂 Ş 昂 Ş 뭥 Ś 昂 8 Sequence 1, Application US/08742877 Patent No. 6046380 Matches Best Query Match GENERAL INFORMATION: APPLICANT: CLARK, Anthony J. TITLE OF INVENTION: DNA SEQUENCES NUMBER OF SEQUENCES: 14 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 NEW YORK AVENUE, NW, SUITE 600 CITY: WASHINGTON SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/742,877 PEATURE : NAME/KEY : COMPUTER READABLE FORM: PEATURE : MOLECULE TYPE: mRNA MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Local APPLICATION NUMBER: FILING DATE: 01-NOV LOCATION: TYPE: nucleic acid COUNTRY: USA ZIP: 20005-3934 STATE: DC NAME/KEY: TOPOLOGY : STRANDEDNESS: single LOCATION: -ENGTH: 2662 1381 1321 1414 2782 2722 947; 61 1 ANTCANAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAAATTAACAGGGCCTCTCAC 60 Similarity CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380 TTCTGGTTCAT 2792 CITCIAGAGAGITIGCIGACCAACIGACGIAIGITICCCCITIGIGAATIAAIAACIGGIG 2781 TTCTGGTTCAT 1391 2802 base pairs Conservative від\_рерtide 30..167 mat\_peptide 168..1412 CDS linear 30..1412 81.2%; Score 1385.8; 68.2%; Pred. No. 0; ... 440; Mismatches 0623.0470001/REF Version #1.30 DB N ;: ω Indels Length 2802 °; Gaps 0 Ş Ś 昂 Ş 片 Ş 昂 Ś 뭉 Ş 昂 Ş 昂 Ş 문 Ş Ş Ş 昂 ą 昂 Ś 昂 ą 8 昂 昂 Ş 昂 昂 昂 昂 Ş 뭉 Ş 昂 2374 1714 1654 1141 2494 2434 2314 2194 2134 2074 1834 1774 1534 1081 1021 2254 2014 1954 1894 1594 196 106 841 721 661 601 541 481 421 361 301 241 181 781 121 TTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATGGAA ATCATTGTAACTAAAAAAGCTGACATTGACCCCAGACATATTGTACTCTTTCTAAAAATAA UAUGCGUGUGUGUAGACACACGCAUACACACAUAUAAUGGAAGCAAUAAGCCAUUCUA AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC UCUAUCACAAGGCCAGUACCACUCAUGAAGAAAGAACACAGGAGUAGCUGAGAGGCUA UCUCCAACCAAAAACAUCAAUGUUUAUUAGUUCUGUAUACAGUACAGGAUCUUUGGUCUAC CAACUAACUCACUCAAUUUUCCCUCCUUAGCAGCAUUCCAUCUUCCCGAUCUUCCUUGCU CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT CCACUAGAGGAAUAUAAUGUGUUAGGAAAUUACAGUCAUUUCUAAGGGCCCAGCCCUUGA CCACTAGAGGAATATATGTGTTAGGAAATTACAGTCATTCTAAGGGCCCAGCCCTTGA = : | •• 1020 2073 480 1200 2553 1140 2493 1080 2433 2373 960 900 840 2193 .2133 720 660 2013 600 1953 1893 1833 1773 1713 1653 240 1593 1533 2313 2253 780 540 420 360 300 180

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Qy       291       TCCACTATGGCAACTAACTCACTCACTCACTCTTAGCAGCATTCCATCTCCCCGAT       350         Db       241       TCCACTATGGCAACTAACTCACTCAATTTTCCTCCTTAGCAGCATTCCATCTTCCCGAT       300         Qy       351       CTTCTTTGCTTCTCCAACCAAAACATCAATTTTTCCTCCTTAGCAGCATTCCATCTTCCCGAT       300         Qy       351       CTTCTTTGCTTCTCCAACCAAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC       410         Db       301       CTTCTTTGGTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC       360         Qy       411       TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAACAACAGGAGTAGC       470         Db       361       TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAAAAAAA	Qy       111 GATCATTGCTTTTTCTCTCTTTACAGAGAATTTACCTGACCAAATTGATTA 170         Db       61 GATCATTGCTTTTTCTCTCTTTACAGGGAAATTTCATATTTACCTGAGCAAATTGATTA 120         Qy       171 GAAAATGGAACCACTAGAGGAATATACGGGAAATTTCATATTTACCTGAGCAAATTGATTA 120         Qy       171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230         Db       121 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 180         Qy       231 CAGCCCTTGACAAATTGTGAAGTAAATTGTGTAAGTGTTCCCACTCTGTCCAACAATACGATACTATGGTTC 290         1	<pre>i ORGANISM: Homo sapiens US-09-328-925-3 Ouery Match 74.6%; Score 1273; DB 3; Length 1273; Best Local Similarity 100.0%; Pred. No. 1.6e-308; Matches 1273; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATACATTCTAT 110                                    </pre>	<pre>Sequence 3, Application US/09328925 Patent No. 6610906 GENERAL.INPORMATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Kotoku TITLS OP INVENTION: Nucleotide Sequences for Gene Regulation and Methods of TITLS OP INVENTION: Use Thereof PILE REFERENCE: UN-03603 CURRENT PILLING DATE: 1999-06-09 SOPTWARE: Patentin Ver. 2.0 SEQ ID NO 3 CURRENT PILLING DATE: 1999-06-09 LENGTH: 1273 CURRENT I Sec DATE: 2.0 </pre>	Qy       1381 TICIGGTIC 1389         pb       2794 UUCUGGUUC 2802         RESULT 8         UUS-09-328-925-3	Qy       1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT 1320         Db       2674 UUUCGGUUUCGUGUUCACCAUGGAACAUUUUGAUUAUAGUUAAUCCUUCUAUCUUGAAU 2733         Qy       1321 CTTCTAGAGAGTTGCTGACCGAACGGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG 1380         Db       2734 CUUCUAAGAGAGTTGCTGACCGAACGGACGTATGTTTCCCCTTGTGGAATTAATAAACTGGTG 2793	Db       2554 AGUUGCCUAGACCAGAGGACAUAAGUAUCAUGUCUCCUUUAACUAGCAUACCCCGAAGUG       2613         Qy       1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT       1260         Db       2614 GAGAAGGGUGCAGCAGGCUCAAAGGCAUAAGUCAUCCAAUCAGCCAACUAAGUUGUCCU       2673
RESULT 9 US-09-328-925-83 Sequence 83, Application US/09328925 Patent No. 6610906 GENERAL INFORWATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Kotoku TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of TITLE OF INVENTION: Use Thereof FILE REFERENCE: UM-03603 CURRENT APPLICATION NUMBER: US/09/328,925 CURRENT FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 84 SOFTWARE: Patentin Ver. 2.0	Db       1141       CCCCGAAGTGGGAGGGGGGGGGGGGGGGGGGGGGGGGGG	Db       961       CTAAAAAATAATAATAATAATAATAATAATAATAATAATA	831 761 891 841 951 901	Qy       711       AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	$ \begin{array}{llllllllllllllllllllllllllllllllllll$	Db       421 TGAGAGGCTAAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT       480         QY       531 TTACCTTTTCCAAATCCCAATCCCCAATCCACTTTTTTCTCTTTTCTCTTTTCTCCTC

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952 GATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTC	Qy 832 GTGTGTGTGTATGCGTGTGTGTATGCACACACGCATACACACAC		Qy         652         ACAGITATACATGITCTATCAAACCCAGACTIGCTICCATAGIGGAGACTIGCTITCAGA         711           B	Qy         592         TITACCCTCCATGGTCGTTAAAGGAGAGAGGAGGAGCATCATTCTGTTATACTTCTGTAC         651           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy         532         TACCTITICCAAATCCCCAAATCAGTITITCTCTITCTTACTCCCTCTCCCT         591           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy         472         GAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTT         531           Db	Oy         412         TTGGTCTACTCTATCACAAGGCCAGTACCACCACTCATGAAGAAAGA	QY         352         TICTTIGCTICICCAACCAAAACATCAAIGITTAATAGITCIGTATACAGTACAG	OY 292 CGACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATC 351 	Qy         232         AGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCT         291	Oy         172         ADAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCC         231           0Y	OY       112       ATCATTGCTTTTCTCTTTACAGGGGAGAAATTTCATATTTTACCTGAGCAAATTGATTAG       171         OY	OY         52         GCCTCTCACTAACTAATCACTTTCCCATCTTTTGTAGATTTGAATATATACATTCTATG         111           OY	Query Match 74.5%; Score 1272; DB 3; Length 1272; Best Local Similarity 100.0%; Pred. No. 2.9e-308; Matches 1272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-328-925-83	10
291 241		61 171	g 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATAT	125-76 .ch 74.5%; Score 1271.4; DB 3; Length 1273; .l Similarity 99.9%; Pred. No. 4.1e-308;	TYPE: DI ORGANISI FEATURE OTHER II	NUMBER OF SEQ ID NOS: 84 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 76 LENGTH: 1273	고고입었	GENERAL APPLICA APPLICA TITLE O	RESULT 10 US-09-328-925-76 ; Sequence 76, Application US/09328925 ; Patent No. 6610906	1261	1201 1312	1141	1081		1012 TAAAAAIAAIAAIAAIAAIAAIAAIAAIAAIGELAAAAGAAAGAAGAGAGAGAGTCTTCGCAATCTACAGC 961 TAAAAATAATAATAATAATGACTAACAGAAAGAAGAGAACCGTTCGTT	901

RESULT 11 US-09-328-925-77 , Sequence 77, Application US/09328925	Db 1261 TATCTTGAATCTT 1273	iggiri 1323	GAAGTGGAGAAGGGTG TGTCCTTTTTCTGGTTT 	1191 CCCCCGAAGTGGAGAAGGGTGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT	Oy 1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190 	CY         1071         CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTCAGGCACTGTTCAGAGCCAAGC         1130	961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTT	DD 901 AGATTGGCATATCATTGTAACTAAAAAGCTGACATTGACCCCAGACATATTGTACTCTTT 960 01 Agattggcatatcattgtaactaaagaagaagaagaacacatattgtactcttt 960	Db 841 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 900 OY 951 AGATTGGCATATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010	781 891	831 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGACACACAC	Oy         771         Aggttatettatatatatatatatatatatatatatatata	Oy         711         AACATAGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	601 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG	Db 541 TITTACCCTCCATGGTCGTTAAAGGAGAGAGAGGGGGAGCATCATTCTGTTATACTTCTGTA 600 Oy 651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710	591 TITTACCCTCCATGGTCGTTAAAGAGAGAGAGGGGGGGGGCATCATTCTGTTATACTTCTGTA 6	QY       \$31       TTACCTTTTCCAAATCCCCAATCCCCAAATCAGTTTTTCTTTC	DS 421 TGAGAGGCTAAAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530 421 TGAGAGGCTAAAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 480	361 TTTUGTICITICITICITICITICITICITICITICITICITIC	411 ·	OY       351       CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC       410         Dh       301       CTTCTTTGCTTCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC       410	
DD 661 AACATAGGGATGAAGTAAGGTACCTGAAAAGTTTGGGGGAAAAGTTLC11CAAGAGAG1.20 Qy 771 AAGTTATTTTATATATATATATATATATATATATATATA		Qy         651         CACAGETTATACATGETCEATACAAGACCEAGACETECCEATAGETGGAGACACETECETECEAG         710           Db         601         CACAGETTATCAACCEAGACETECCEATAGETGCAEACETECEATAGETGGAGACETECETECEATAGETGGAGACETECEATAGETGGAGACETECEATAGE         660	Dy 591 TTTTACCCTCCATGGTGGTAAAGGAGAGTGGGGAGCATCATTCTGTTATACTTCTGTA 650 	481 TTACCTTTTCCAAATCCCCAAATCAGTTTTTCTCTTTCTT	Db         421         TGAGAGECTAAAACTCATCAATAAAAAAAACACTACTCCTTTTCCTCTACCCCTATTCCTCAATCTT         480           Cy         531         TTACCTTTTCCAAATCCCCAATCCCCCAATCAGTTTTTCTCTTTCTT	Db 361 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAAAAAA	411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGA	$Oy \qquad 351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410 \\                                    $	Oy         291         TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT         350           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII			Db 61 GATCATTGCTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120 0y 171 GAAAATGGAACCACTAGAGGGAGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230	Db 1 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATAACATTCTAT 60 QY 111 GATCATTGCTTTTTCCTCTTTACAGGGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170	51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATAT	Query Match 74.5%; Score 1271.4; DB 3; Length 1273; Best Local Similarity 99.9%; Pred. No. 4.1e-308; Matches 1272; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	, OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-328-925-77	TYPE: DNA ORGANISM: Artificial Sequence FEATURE:	; NUMMAEK OF SEQ ID NOS: 84 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 77 : LENGTH: 1273	CURRENT ELLING DATE: 1999-06-09	ITITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of ITILE OF INVENTION: Use Thereof	Patent No. 6610906 GENERAL INFORMATION: APPLICANT: Kurachi, Kotoku	

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Db 61 GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 120	Db 11 GACCICICACIAACTAACAACTICCCAICITICAIAATTIACCIGAGAAAATTGAIIA 170 OY 111 GATCAITICCITITICICITIACAGGGGAGAAATTICAIATTITIACCIGAGCAAATTGAIIA 170	51 GECETETEACTAACTAATCACTTTCCCATCTTTGTTAGATTIGAATATATATACATTCTAT	Query Match 74.4%; Score 1269.8; DB 3; Length 1273; Best Local Similarity 99.8%; Pred. No. 1e-307; Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-328-925-78	; TYPB: DNA ; ORGANISM: Artificial Sequence ; FEATURE:	; SOFTWARE: PatentIN Ver. 2.0 ; SEQ ID NO 78 ; LENGTH: 1273	CURRENT FILING DATE	; GENERAL INFORMATION; ; APPLICANT: Kurachi, Kotoku ; APPLICANT: Kurachi, Sumiko ; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of	1 i i i i i i i i i i i i i i i i i i i	Db 1261 TATCTTGAATCTT 1273	OY 1311 TATCTTGAATCTT 1323	ANGTIGTECTTTTCTGGTTTCGTGTTCACCATGGAACATTTGATTATAGTTAATCCTTC	1141	1191	OY       1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGAGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 1021 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1080	961	1011	Db 901 AGATTIGGCATATCATTIGTAACTAAAAAAGCTIGACATTGACCCAGACATAATGTACTCTTT 960	841 ÁGCCÁTTCTAÁGÁGCTTGTAIGGTTAIGGAGGTCTGACTAGGCATGATTTCACGAAGGCA		811 TETETETETETETETETETETETETETETETETETET	DD 721 AAGTTATTTATATATATATATATATATATATATATATAT
	4 4	10 da		07 10	Qy 10	Ag da	dd Ad	yo Yo	29 <del>4</del>	DP QX	da		40 70	ם מס	Q D		р УУ 4			27 AU		•	
251 AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310	191 CCCCGAAGTGGAGAAGGGTGCAGCAGCTCAAAGGCATAAGTCATTCCATTCAATCAGCCAACT 1250			961 CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTT	CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTT	951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010 	891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGTCTGACTAAGGCAYGATTTCACGAAGGCA 950 		771 AAGTTATTTTATATATATATATATATATATAAAATATATAATAT	711 AACATAGGGATGAAGTAAGTGCCTGAAAAGTTTCGGGGGAAAAGTTTCTTTC	CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCCAG		591 TTTTACCTCCATGGTCGTTAAAGGAGAGAAGATGGGGAGCATCATTCTGTTATACTTCTGTA       650	<b>υ</b>	421 TGAGAGGGCTAAAAACTCATCAAAAAAACACTACTCCITTCCTCTACCCIAIICCICAAICCICAAACCAAAACAACTACTCCITTCCTTTCCTTACTCCCCCCCC		411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGA			291 TCCACTATGCAACTACTCACTCAATTTTCCCTCCTTACAGCATCCATC	CAGCCCTTGACAAAATTGTGAAAGTTAAAATTCTCCCACTCTGTCCAATCAAATACTATGGTTC 24		171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 230

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QY       291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTAGCAGGATTCCATCTTCCCATCTTCCCAT       350         Db       241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTAGCAGGATTCCATCCA	Ouery Match Best Local Similarity       74.2%; Score 1266.6; DB 3; Length 1273; Matches 1269; Conservative       0; Mismatches 4; Indels       0; Gaps       0;         OV       51 GGCCTCTCACTAACTAATCACTTTCCACTCTTTGTTAGATTTGAATATACATTCTAT       10       11 <td< th=""><th>SULT 13 Sequence 79, Application t Patent No. 6610906 GENERAL INFORMATION: APPLICANT: Kurachi, Kuto TITLE OF INVENTION: Nucli TITLE OF INVENTION: Nucli TITLE REFERENCE: UM-03603 CURRENT APPLICATION NUMBE CURRENT FILING DATE: 1999 NUMBER OF SEQ ID NOS: 84 SOFTWARE: PatentIn Ver. 2 LENGTH: 1273 TYPE: DNA ORGANISM: Artificial Sec PEATURE: INFORMATION: DESCT</th><th>Db       1201       AAGTTGTCCTTTTCTGGTTTCCGGTTTCACCATGGAACATTTGATTATAGTTAATCCTTC       1260         Qy       1311       TATCCTGAATCTT       1223         Db       1261       TATCCTGAATCTT       1223         Db       1261       TATCCTGAATCTT       1273</th></td<>	SULT 13 Sequence 79, Application t Patent No. 6610906 GENERAL INFORMATION: APPLICANT: Kurachi, Kuto TITLE OF INVENTION: Nucli TITLE OF INVENTION: Nucli TITLE REFERENCE: UM-03603 CURRENT APPLICATION NUMBE CURRENT FILING DATE: 1999 NUMBER OF SEQ ID NOS: 84 SOFTWARE: PatentIn Ver. 2 LENGTH: 1273 TYPE: DNA ORGANISM: Artificial Sec PEATURE: INFORMATION: DESCT	Db       1201       AAGTTGTCCTTTTCTGGTTTCCGGTTTCACCATGGAACATTTGATTATAGTTAATCCTTC       1260         Qy       1311       TATCCTGAATCTT       1223         Db       1261       TATCCTGAATCTT       1223         Db       1261       TATCCTGAATCTT       1273
RESULT 14 US-09-328-925-82 ; Sequence 82, Application US/09328925 ; Patent No. 6610906 ; Patent No. 6610906 ; Patent No. 6610906 ; FILCANT: Kurachi, Kotoku ; APPLICANT: Kurachi, Sumiko ; TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of ; TITLE OF INVENTION: Use Thereof ; FILE REFERENCE: UM-03603 ; CURRENT FILING DATE: 1999-06-09 ; MUMBER OF SEQ ID NOS: 84 ; SOFTWARE: PatentIN Ver. 2.0 ; SEQ ID NO 82 ; LENGTH: 1272 ; TYPE: DNA ; ORGANISM: Artificial Sequence ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-328-925-82 ; Query Match 73.9%; Score 1261; DB 3; Length 1272;	Qy       1071       CTAGTAGAGACTTTGAGGAGAATTCAACAGTGTCTCCAGGAGTGTCTAGAGGCAAGC         Db       1021       CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTCTCTCAGCAGTGTTCAGAGCCAAGC       1080         Qy       1131       AAGAACTTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCAGAGCCAAGC       1080         Qy       1131       AAGAACTTGAAGTTGGCCTAGACCAGAGGACATAAGTATCATGTCTCCAGCAAGCA	661       AACATAGGGATGAAGTTAAGTTAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCAGAGATT         771       AAGTTATTTTATATATATATATATATATATATATATATA	$ \begin{array}{llllllllllllllllllllllllllllllllllll$

Local Sinitarity 99.9%, pred. No. 1.66-305, rades 1. dap 1.
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1       1707       100.0       1707       3       US-09-680-10727       Sequence 7, Appli         2       1701       98.5       98.6       44752       8       US-10-741-600-17553       Sequence 17553, Ap         4       1391       81.5       1400       9       US-10-741-600-17553       Sequence 17553, Ap         5       1391       81.5       1400       10       US-11-060-756-6209       Sequence 1937, Ap         6       1391       81.5       1400       10       US-11-060-756-6209       Sequence 2, Appli         10       1391       81.5       2804       5       US-10-133-907-2       Sequence 2, Appli         11       1391       81.5       2804       9       US-10-056-157-357       Sequence 3, Appli         12       1376.6       80.6       2773       6       US-10-744-600-3       Sequence 1, Appli         13       1376.6       80.6       2777       8       US-10-741-600-2       Sequence 2, Appli         14       1376.6       80.6       2777       8       US-10-741-600-2       Sequence 1, Appli         15       1376.6       80.6       2777       8       US-10-741-600-2       Sequence 2, Appli         16	ed by chance to have f the result being p ore distribution. Descripti	Post-processing: Minimum Match 0% Maximum Match 100 Listing fittet 45 summaries Database : Published Applications NA_Main:* 1: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:* 3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:* 4: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:* 5: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:* 6: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:* 9: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:* 10: /cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Copyr eic - nucleic se April 1 score: 1707 e: 1 aatga table: IDENTIT Gapop 1 d: 9793542 d: 9793542
1707; CONSETVALVE 0; PISMACCIES 0; LINELS 0; COPP AATGAAAGATGATTTCCAAGGTTAALTCATTGGAATTGAAAATGAAAGGGGCCTCTCAC 60 1 AATGAAAGATGGATTTCCAAGGTTAALTCATTGGAATTGAAAATGAAAATGAACGGCCCTCTAC 60 61 TAACTAATCACTTTCCCATCTTTTGTTAGATTGGAATTGAATATAACAGGGCCCATCATTGCT 12 61 TAACTAATCACTTTCCCATCTTTTGTTAGATTGGAATATATAT	RE: Patentin version 3.0 NO 7 DNA DNA ISM: HomoSapien -901-7 atch 100.0%; Score 1707; DB 3; Length 1707; atch 100.0%; Pred. No. 0; Tatala 0. Gang 0	-901-7 e 7, Application US/ e 7, US20020076798A1 INFORMATION: ANT: Miao, Carol ANT: Kay, Mark OF INVENTION : Liver: OF INVENTION : Liver: EFERENCE: UOFW-1-173: EFERENCE: UOFW-1-173: FILING DATE: 2000-06 FILING DATE: 2000-06 FILING DATE: 2000-06	ALIGNMENTS	24       200.6       11.8       201       8       US-10-741-600-18209       Sequence 18209, A         25       200.6       11.8       201       8       US-10-741-600-18309       Sequence 12761, A         26       172.4       10.1       422       3       US-09-960-352-12761       Sequence 12761, A         27       160       9.4       1928       1.14       1928       Sequence 12761, A         29       159       9.3       1548       3       US-09-960-352-112761       Sequence 6, Appli         30       94.2       5.5       370       3       US-09-950-9510-911-6       Sequence 6, Appli         31       89       5.2       201       8       US-10-741-600-2148       Sequence 11540, A         32       86.4       5.1       1555       4       US-09-925-065A-308075       Sequence 2148, Ap         40       85       5.0       201       8       US-09-925-065A-308075       Sequence 2177, Ap         41       85       5.0       201       8       US-09-925-065A-308075       Sequence 1867, Ap         42       85       5.0       201       8       US-09-925-065A-308075       Sequence 1867, Ap         5       Sequence <t< td=""></t<>

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	321 CTTCTAGAGAGTIGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG	
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	GAGAAGGGTGCAGCAGGGTCAAAGGCATAAGTCATTCCAATCAACCAAC	
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	901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960	Db
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	01 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCCGATCTTTGCT	}

Sequence 2125, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-06-14
PRIOR FILING FILING DATE: 2000-06-14
PRIOR FILING PRIOR FILI 昂 8 昂 Ş 昂 8 Ş 昂 片 Ś ; FEATURE: ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 K02402 US-09-880-107-2125 US-09-880-107-2125 멂 Ş 昂 R 昂 Ş 昂 Ş 昂 Ş RESULT Query Match 99.7 Best Local Similarity 99.9 Matches 1703; Conservative ы 34573 34513 34453 34393 1681 1621 1621 1561 181 121 1681 1561 1501 1501 1441 1441 241 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240 GAGGTTAGGAGTTTCAGGCCAAGCTTA 1707 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 34632 TTTTCTCTTTTACAGGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180 TAACTAATCACTTTCCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT CCACTAGAGGAATATAATGTGTTAGGAAAATTACAGTCATTTCTAAGGGCCCCAGCCCTTGA 34572 TTTTCTCTTTTACAGGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA GCCCAGTGGCTCACGCCTATATAATCCCCAGCACTTCTGGAGGCCCAAGGTGGGCGGATCACCT 1680 GAGGTTAGGAGTTTCAGGCCAAGCTTA 1707 GCCCAGTGGCTCACGCCTATAATCCCCAGCACTTCTGGAGGCCCAAGGTGGGCGGATCACCT AATATATTTTTGTCTTCGCATATAAGTATAAAATAAACATATTTTTAAAATTTCTTGGCTGG reccccaacercaceccaeccaecercaercreeraerrectreerraerrectreaerc 99.78; 99.98; ; Score 1701.8; ; Pred. No. 0; 0; Mismatches DB 3; 2; Indels Length 38059; 0; Gaps 300 120 34392 34512 34452 60 1680 1620 1560 1500 1500 1620 1560 <u>,</u>

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1381 TTCTGGTTCATACCTTGGCTTTTTTGTGGATTCCATTGATGTGAATCAGTCACCCTGTATT 1440

Db       37485       THTPCTCTTACAGGGAGAATTCATATTCATATCAGCAAATTCAATCAA	1201       GAGAAGAGGTIGCAGCAGAGGTIGCATCAATCAGCCALCAACCAAGTIGTCCL       1201         35533       GAGAAGGTIGCAGCAGGTGCAGGCTCAAAGGCATTAAGTCATTCCAATCAGCCAACTAAGTTGTCCT       35592         1261       TTTCTGGTTTCGTGTTCAACGAGGCACATTATGACTAAGTCATTCCAATCAGCCTAACTAA	ይ <del>የ</del> ይ የ ይ <del>የ</del>
00       5/365       AALGMAGAGGAATTCCCATCTTTGTTAGATTGAATATATACATTCTATGATCATTGCT       120         0y       61       TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT       120         0b       37425       TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT       37484         0y       121       TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGGCAAATTGAATAGGAAATGGAAA       180         0y       121       TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGGCAAATTGATAGAATGGAAA       180	35413 CTTTGAGGAAGAAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGGAAGTTGA 1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGCAGTGTTCAGAGCCAAGCAAG	о Су Су
-10-741-600-17553 Query Match Beet Local Similarity 99.6%; Pred. No Beet Local Similarity 99.6%; Pred. No Matches 1699; Conservative 2; Misma 1 AATGAAAGATGGATTTCCAAGGTTAATT 1 AATGAAAGATGGATTTCCAAGGTTAATT 1	961 35293 35353 1081	67 8 67 8 67 67 8 67 8 67
SEQ ID NO 1753 IERGTH: 44752 ICRGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: (1)(44752)	841       TATECGTETETAGCACACACGCATACACACACACACACACACACACACAC	8, 92 B 92 B
GENERAL INFORMATION: APPLICANT: CARGILL, Michele et al. TITLE OF INVENTION: GENERIC FOLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF FILLE REFERENCE: CLOOL499 CURRENT PAPLICATION NUMBER: US/10/741,600 CURRENT FILING DATE: 2003-12-22 NUMBER OF SEQ ID NOS: 73997 NUMBER OF SEQ ID NOS: 73997	721       TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Db       36013       GAGGTTAGGAGTTTCAGGCCAGCCT       36037         RESULT 3       US-10-741-600-17553       US/10741600         ; Sequence 17553, Application US/10741600       is/20050026169A1	601       CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA       660         34933       CATGGTCGTTAAAGGAGAGTGGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA       34992         661       CATGGTCGTTAAAGGAGAGTGGCTGCCTTCCATAGTGGAGACTTGCTTTTCAGAACATTAGGGA       720         1	40 67 67
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0y 361 TCTCCAACCAAAACATCAATGTTTAATAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420	QY       301       CAACTAACTCAATTTTCCCTCCTTAGCAGCATCCATCTTCCCGATCTTCTTTGCT       360         Db       310       CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATCCATC	Qy 241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 300 	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Qy 121 TTTTCTCTTTACAGGGAGAAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 180 	Qy 61 TAACTAATCACTTTCCCATCTTTGTTAGATTGAATATATACATTCTATGATCATTGCT 120 	Qy 1 AATGAAAGATGGATTTCCAAGGTTAATTCATTCGAATTGAAAATTAACAGGGCCTCTCAC 60 	Query Match 81.5%; Score 1391; DB 9; Length 1400; Best Local Similarity 100.0%; Pred. No. 0; Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; TYPE: DNA ; ORGANISM: Homo sapiens US-10-956-157-5592	NUMBER OF SEQ ID NOS: 319805 SOFTWARE: PatentIn version 3.2 LENGTH: 1400	TITLE OF INVENTION: HUMAN OSTEORATHRITIS AND HUMAN PROTEASES FILE REFERENCE: 031896-043000 (AM 101081) CURRENT APPLICATION NUMBER: US/10/956,157	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Wyeth APPLICANT: Mounts, William APPLICANT: Mounts, William APPLICANT: Mounts, William	RESULT 4 US-10-956-157-5592 ; Sequence 5592, Application US/10956157 ; publication No. reconcentations.	Db 39043 GAGGTTAGGAGTTTCAGGCCAGCCT 39067	1681 CACCENTRACACCENTRACCCAGCACCTTCTGGAGGCCAAGGTGGGCGGATCACCT		38863	1501 TGCCCCAACCTCACCCCCAGCCAGGCCTCACTCTTGCTAGTTCCTTTAGTTCTTTAGTC	OY 1441 TGATGATGGATGGGACTACTGACAAAATCACTCTGACCCTGCCAAGCTGCCTGC	DD 38743 TICIGGIICATACCIIGGCIITITIGIGGATICCAIIGANGTGAAICAGICACCCIGIATI 38802

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RESULT 5 US-11-060-756-1937	QY 1381 TICTGGTICAT 1391              Db 1390 TICTGGTICAT 1400	Oy         1321         CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACT	OY 1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAT	Oy         1201         GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT	Oy         1141         AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCCTTTAACTAGCATACCCCCGAAGTG           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         1081         CTTTGAGGAAGAATTCAACAGTGTGTTCAGCAGTGTTCAGAGCCAAGCAAG	Qy         1021         TAATAATAATGCTAACAGAAAGAGAAGGAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA           Qy	Oy         961         ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy         901         agagettigtategittategaggetetgactaggeatgatticaceaaggeaagattegeat           0y	Oy         841         TATGCGTGTGTGTGTAGACACACACACACACACATATAATGGAAGCAATAAGCCATTCTA           Oy	Oy         781         ATATATATATATATATATATAAAAATATATAATATAA	Qy         721         TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	Oy         661         CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA           0y	Qy         601         CATEGETCETTAAAGGAGAGATGGGGAGCATCATTCTCTTATACTCTCTATACACAGTTATA           Qy	Oy         541         CAAATCCCCAATCCCCCAAATCAGTTTTTTCTCTTTTTTACTCCCTCTCTCCCCTTTTACCCTC           Oy	Oy         481         AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC           0y	OY         421         TCTATCACAAGGCCAGTACCACACTCATGAAGAAGAACACAGGAGTAGCTGAGAGGCTA           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 370 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC
$\begin{array}{cccccccccccccccccccccccccccccccccccc$			1320         Qy         541         CARATCCCARTCCCCARATCAGTTTTTCCCTTTCCTACTCCCCCTCTCCCCTTTACCCTC           1329         Db         550         CARATCCCCARTCCCCARATCAGTTTTTCTCTTTCTTACTCCCTTTCCCCTTTACCCCCCTTTACCCCC	1260         Oy         481         AAACTCATCAAAAACACTACTCCTTTCCCTCTACCCTATTCCTCAATCTTTTACCTTTTC           1269         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1200         Qy         421         TCTATCACAAGGCCAGTACCACACTCATGAAGAAACAACAGGGTAGCTGAGAGGCTA           1200         Db         1000 <t< td=""><td>1140         Qy         361         TCTCCAACCAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC           1140         Db         370         TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC           1149         Db         370         TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC</td><td>1080         Qy         301         CAACTAACTCAACTCCAATTTTCCCTCCCTTAGCAGCATTCCATCTTCCCGATCTTCCTTGCT           1089         Db         310         CAACTAACTCAACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT</td><td>1020         Qy         241         CANANTTGTGANGTTANATTCTCCACTCHETCCARCAGNACTANGGTTCTCCACTATUG         30           1029         Db         250         CANANTTGTGANGTTANATTCTCCACTCHETCCARCAGNACTATGGTTCTCCACTATUG         30           1029         Db         250         CANANTTGTGANGTTANATTCTCCACTCHETCCARCAGNACTATUGGTTCTCCACTATUG         30</td><td>960 OY 181 CCACTAGAGGAATATAATGTGTTAGGAATTACAGTCATTTCTAAGGGCCCAGCCTTGA                                    </td><td>900         0y         121         TITITCTTTTACAGGGAGAATTTCATATTTAACCTGAGCAAATTGATTAGAAAATGGAA           909         Db         130         TITITCTCTTTACAGGGGAGAATTTCATATTTAACCTGAGCAAATTGATTAGAAAATGGAA</td><td>84.0         Oy         61         TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGTT           84.0         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII</td><td><math display="block">\begin{array}{cccccccccccccccccccccccccccccccccccc</math></td><td>720 Query Match Best Local 1 Matches 139</td><td>699</td><td>CTC 600 ; NUMBER OF SEQ ID NOS: 303284     ; SOFTWARE: PatentIn version 3.2 CTC 609 ; SEQ ID NO 1937 CTC 609 ; LENGTH: 1400</td><td>540 ; TITLE OF INVENTION: TArget ; FILE REFERENCE: AMIO1083 (0: 549 ; CURRENT APPLICATION NUMBER: ; CURRENT FILING DATE: 2005 (</td><td>480</td><td>429</td></t<>	1140         Qy         361         TCTCCAACCAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC           1140         Db         370         TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC           1149         Db         370         TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC	1080         Qy         301         CAACTAACTCAACTCCAATTTTCCCTCCCTTAGCAGCATTCCATCTTCCCGATCTTCCTTGCT           1089         Db         310         CAACTAACTCAACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT	1020         Qy         241         CANANTTGTGANGTTANATTCTCCACTCHETCCARCAGNACTANGGTTCTCCACTATUG         30           1029         Db         250         CANANTTGTGANGTTANATTCTCCACTCHETCCARCAGNACTATGGTTCTCCACTATUG         30           1029         Db         250         CANANTTGTGANGTTANATTCTCCACTCHETCCARCAGNACTATUGGTTCTCCACTATUG         30	960 OY 181 CCACTAGAGGAATATAATGTGTTAGGAATTACAGTCATTTCTAAGGGCCCAGCCTTGA 	900         0y         121         TITITCTTTTACAGGGAGAATTTCATATTTAACCTGAGCAAATTGATTAGAAAATGGAA           909         Db         130         TITITCTCTTTACAGGGGAGAATTTCATATTTAACCTGAGCAAATTGATTAGAAAATGGAA	84.0         Oy         61         TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGTT           84.0         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	720 Query Match Best Local 1 Matches 139	699	CTC 600 ; NUMBER OF SEQ ID NOS: 303284     ; SOFTWARE: PatentIn version 3.2 CTC 609 ; SEQ ID NO 1937 CTC 609 ; LENGTH: 1400	540 ; TITLE OF INVENTION: TArget ; FILE REFERENCE: AMIO1083 (0: 549 ; CURRENT APPLICATION NUMBER: ; CURRENT FILING DATE: 2005 (	480	429

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US-11-060-756-6209 Ouery Match 81.5%; Score 1391; DB 10; Length 1400; Best Local Similarity 100.0%; Pred. No. 0; Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60 	ŝ	RESULT 6 US-11-060-756-6209 Sequence 6209, Application US/11060756 Publication No. US20050221354A1 GENERAL INFORMATION: APPLICANT: Wyeth APPLICANT: Wounts, William Martin APPLICANT: Wounts, William Martin TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Target Genes TITLE OF INVENTION: Target Genes	1381 TICIGGITICAT 1391                1390 TICIGGITICAT 1400	OY       1321 CTTCTAGAGAGTIGCCGACCGACCGACGGACGTATGTTTCCCTTIGTGAATTAATAAACTGGTG       1380         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy       1261       TITCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATGCTTCTATCTTGAAT       1320         Db       1270       TITCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATGCTTCTATCTTGAAT       1329	Oy         1201         GAGAAGGETGCAGGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT         1260         1210         Image: Comparison of the second c	Oy       1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG       1200         Oy	Qy         1081         CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTCTCAGAGCCAAGCAAG	Qy 1021 TAATAATGATAAGAGAAAGAGAAGAGAGAGAGCGTTCGTT	Oy 961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020 	Qy       901       AGAGCTTGTATCGTTATCGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT       960         Db       910       AGAGCTTGTATCGTTATCGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT       969	Oy 841 TATGCGTGTGTGTGTAGACACACACACACACACATATAATGGAAGCAATAAGCCATTCTA 900 	Oy         781         ATATATATATATATATATATATATATATATATATATAT
8	<u> </u>	ት 6	Db Qy	<b>Å</b>	A Vo	ap da	5 Q	5 Q	Åð V	DP QY	Qү	DP QX	da Ao
Trataataatigetaacagaagaagaagaaccgttegttegeaatetacagetagaga 		721       TGAAGTAAGGTGCCTGJAAAGTTTGGGGGGAAAAGTTTCTTTCAGAGAGTTAAGTTAAGTTATTTT       780         730       TGAAGTAAGGTGCCTGJAAAAGTTTGGGGGGAAAAGTTTCTTTCAGAGAGAGTTAAGTTATTTT       780         730       TGAAGTAAGGTGCCTGJAAAAGTTTGGGGGAAAAGTTTCTTTCAGAGAGAGTTAAGTTATTTT       789         781       ATATATATATATATATATATAAAATTGGGGGAAAAGTTTCCTTTCAGAGAGAG	CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 	601 CATGGTCGTTAAAGGAGAGAGGGGGGGGGGGGGGGGGGG	541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTTTTTTTT	481         AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATCCCTCAATCTTTTACCTTTTC         540	421         TCTATCACAAGGCCAGTACCACACACAGAAGAAGAACACAGGAGTAGCTGAGAGGGCTA         480	361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 	301       CAACTAACTCACTCAATTTCCCTCCTAGCAGCATCCATCTTCCCGATCTTCTTGCT       360	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 300 	181         CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA         240	121 TTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATGGAA 180 	61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120 

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361	TAGCAGCATTCCATCTTCCCGATCTTCTTGCT	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 	181	121 TTTTCTTTTACAGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 121 TTTTCTTTTACAGGGAGAAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 1534 TTTTCTTTTACAGGGAGAAATTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA	61 TAACTAATCACTTCCCATCTTTGTTAGATTTGAATATAATACATTCTATGATCATGCT 	Qy       1 AATGAAAGATGGÄTTTCCAAGGTTAATTGAATTGGAAATTGAAAATTAACAGGGCCTCTCAC 60         Db       111111111111111111111111111111111111	300	; SEQ 1D NO 2 ; LENGTH: 2804 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-132-829-2	; PRIOR APPLICATION NUMBER: 607/266,314 ; PRIOR FILING DATE: 2001-04-25 ; NUMBER OF SEQ ID NOS: 5 ; SOFTWARE: Patentin version 3.1	; TITLE OF INVENTION: WITT VESICLE VECCI ; FILE REPERENCE: 6627-PALI70 ; CURRENT APPLICATION NUMBER: US/10/132,829 ; CURRENT FILING DATE: 2002-04-25	, GENERAL INFORMATION: , APPLICANT: Chien, Kenneth R , APPLICANT: Hoshijima, Masahiko , TITLE OF INVENTION: Method to treat hemophilia by hepatic gene transfer of Factor VII	RESULT 7 US-10-132-829-2 ; Sequence 2, Application US/10132829 ; Publication No. US20030044982A1	1390	1330	1270 1321	Db       1210       GAGAAGGGTGCAGCACGAGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTGTCCT       1269         Oy       1261       TTTCTGGTTTCGTGTTCACCATGGAACATTTGATTCAATCAGCCAACTAAGTTGTTCGAAT       1320	Db 1150 AGTIGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTTAACTAGCATACCCCGAAGTG 1209 OY 1201 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 1260	QY 1141 AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200	
RESULT 8 US-10-133-907-2	Qy 1381 TTCTGGTTCAT 1391            Db 2794 TTCTGGTTCAT 2804	Qy         1321         CTTCTAGAGAGTTGCTGACCA  Db         2734         CTTCTAGAGAGTTGCTGACCA	61 74			1081 2494	1021 2434 1081	961 2374	QY 901 AGAGCTTGTATGGTTATGGAG 	OY 841 TATGCGTGTGTGTGTGTAGACACAC 	Oy 781 ATATATATAATATATATATATATA 	Oy         721         TGAAGTAAGGTGCCTGAAAAG           []]]         []]]         []]]         []]]           Db         2134         TGAAGTAAGGTGCCTGAAAAG	Oy         661         CATGTCTATCAAACCCAGACT           Db         2074         CATGTCTATCAAACCCAGACT	Qy         601         CATGGTCGTTAAAGGAGAGAT           [] ]                             []                                       []   Db         2014         CATGGTCGTTAAAGGAGAGAGAGAGAGAGAGAGAGAGAGA	Qy         541         CAAATCCCAATCCCCAATCA	Оу         481         АЛАСТСАТСАЛАЛАСАСТАСТ	Qy 421 TCTATCACAAGGCCAGTACCA 	Db 1774 TCTCCAACCAAAAACATCAATG	
		CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAAAACTGGTG 1300 			261		ы N I	ATCATTGTAACTAAAAAAGCTGACATTGACCCCAGACATATTGTACTCTTTCTAAAAATAA 1020 		NY	atatatatatatatatatatatatatatatatatatat	TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA 720 	$\begin{array}{llllllllllllllllllllllllllllllllllll$	CAAATCCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCCTC 600 	AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540	TCTATCACAAGGCCAGTACCACACTCATGAAGAACAAGAACACGAGTAGCTGAAAAGAC 4 *00 	. щ	

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, QY 721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	Oy         661         CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 601 CATGGTCGTTAAAGAAGAATGGGAAGCATCATTCTGTTATACTTCTGTACACAGTTATA 	541 1954	Oy         481         AMACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC           Db         111111111111111111111111111111111111	Qy         421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA	Qy         361         TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY         301         CAACTAACTCAACTCAATTTCCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCCTTGCT           Db         1/14	Oy         241         CAMAATIGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         181         CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTCTAAGGGCCCAGCCCTTGA	OY 121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 	Oy 61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 	Oy 1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 	Query Match 81.5%; Score 1391; DB 6; Length 2804; Beet Local Similarity 100.0%; Fred. No. 0; Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gap	IENGTH: TYPE: DN ORGANISM IS-10-133-90	; FAAA STELLAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	FILE REFERENCE: 6627-PA1170 CURRENT APPLICATION NUMBER: US/10, CURRENT FILING DATE: 2002-04-25	o treat hemophilia by hepatic gene trans cle vector	; Sequence 2, Application US/10133907 ; Publication No. US20030195223A1 ; GENERAL INFORMATION:
780 QY 1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60	. 720 Query Match 81.5%; Score 1391; DB 9; Length 2804; Best Local Similarity 100.0%; Pred. No. 0; Matches 1391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	2073 U	600 ; NUMBER 2013 ; SEQ ID A ; LENGTH	540 TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES 1953 FILE REFERENCE: 031896-043000 (AM 101081) CURRENT APPLICATION NUMBER: US/10/956,157 CURRENT FILING DATE: 2004-10-04	480	420 RE 1833 ;	360     47     1361     111111111       1773     Db     2794     TICTOGITICAT     2804	300 Db 2734 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG	240 VY 1201 1653 Db 2674 1673 Ov 1321	180     180 <td>120     UY     1111     CANAGE AND AND AND AND AND AND AND AND AND AND</td> <td>60 Db 2494 1473 C 1141</td> <td>1021 TRATATATATATCTAR GAAGGAAGGAAACGTTCGTTTGCTATCAATCTACAGCTAGTAGAAG                               </td> <td>OY 961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020                                    </td> <td>OY 901 AGAGCTTGTATGGTTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960                                     </td> <td>Dy 841 TATGCGTGTGTGTGTGTGTGGAGACACACGCATACACACAC</td> <td>Qy         781 ATATATATATATATATATATATATATATATATATATAT</td> <td>Db 2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC</td>	120     UY     1111     CANAGE AND	60 Db 2494 1473 C 1141	1021 TRATATATATATCTAR GAAGGAAGGAAACGTTCGTTTGCTATCAATCTACAGCTAGTAGAAG 	OY 961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020 	OY 901 AGAGCTTGTATGGTTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT 960 	Dy 841 TATGCGTGTGTGTGTGTGTGGAGACACACGCATACACACAC	Qy         781 ATATATATATATATATATATATATATATATATATATAT	Db 2134 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC

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RESULT 10 RESULT 10 Sequence 40, Application US/10804763 Sequence 40, Application US/10804763 Sequence 40, Application US/10804763 Republication No. US20050118576AL Sequence 40, Application Sequence 1 republication No. US20050118576AL Sequence 40, Application Sequence 1 republication No. US20050118576AL REPUTATE 100 100 republication No. US20050118576AL REPUTATE 100 100 reputation No. US2005011 reputation No. US200501111111111111111111111111111111111	Db       2494       CTTTGAGGAAGAATTCAACAGTGTGTCTCAGCAGGTGTCAGAGGCAAGGAAGAAGTTGA       2553         QY       1141       AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG       1200         Db       2554       AGTTGCCCTAGACCAAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG       2613         QY       1201       GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATGTCTCCTTTCAATCAGCCAACTAAGTTGTCCT       1260         Db       2614       GAGAAGGGTGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCCT       2673         QY       1261       TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTAAGTCATCCTTCTAAGTTGTTCTTGAAAT       1320         Db       2674       TTTCTGGTTTCGTGTTCCGTGTTCACCCAACTGGAACATTTTGATTAATCCTTCTAATCCTTCTAACTGGTG       2733         QY       1321       CTTCTAGAGGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAAATTAAAACTGGTG       1380         Db       2734       CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTCCCTTTGTGAAATTAATAAAACTGGTG       2793         QY       1381       TTCTGGTTCAT       2804       2794         Db       2794       TTCTGGTTCAT       2804       2794

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ş	Qу Db	DP OX	р Q	P Q	DP QA	db Vy	QY VQ	5 Q	5 g	5 Q	Mago	; ; US-(		· · · · ·	·· ·· ·· ·		., ., ., .,	 	RESI
601 CATGGTCGTTAAAGGAGAGAGAGGGGGGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA	541 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCCCCTTTTACCCCTC 	481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTC 	421 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 	361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 	301 CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTGCT 	241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 	181         CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTCTAAGGGCCCAGCCCTTGA	121 TTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA 	61 TAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATAT	1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 	Query Match 81.3%; Score 1387.8; DB 3; Length 2792; Best Local Similarity 99.9%; Pred. No. 0; Matches 1389; Conservative 0; Mismatches 2; Indels 0; Gaps	NAME/KEY: CDS Location: (156)(1400) 19-118-748-1	PEATURB: OTHER INFORMATION: Description of Artificial Sequence: sequence of OTHER INFORMATION: human factor IX-R338A FEATURE:	; SEQ ID NO 1 ; LENGTH: 2792 ; TYPE: DNA ; ORGANISM: Homo sapiens	SARLIER FILING DATE: 1997-07-21 UMBER OF SEQ ID NOS: 2 (OPTWARE: Patentin Ver. 2.0	FILE REFERENCE: 5470-183 URRENT APPLICATION NUMBER: US/09/118,748A URRENT FILING DATE: 1998-07-17	APPLICANT: Scallord, Matter M. APPLICANT: Chang, JinLi ITTLE OF INVENTION: Factor Ix Antihemophilic Factor with Increased Clotting	ALEANT NO. USZOZOOJI799AI	RESULT 11 US-09-118-748-1 ; Sequence 1, Application US/09118748A

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RESULT 12 US-10-349-858-16 Sequence 16, Application US/10349858 Publication No. US20030220247A1 GENERAL INFORMATION: APPLICANT: The Children's Hospital of Philadelphia APPLICANT: HIGH, KATHERINE A. APPLICANT: LIGH, KATHERINE A. APPLICANT: LARSON, PETER J. APPLICANT: LARSON, PETER J. APPLICANT: LARSON, PETER J. APPLICANT: LARSON, DARREL W. TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G TITLE OF INVENTION: ENHANCED GAMMA-CARBOXYLATION OF RECOMBINANT VITAMIN K-DEPENDENT G F RIGH RELICATION NUMBER: US/10/349, 858 F RIGH F RIGHT F RIGHT GAME: 2000-03-16	pp       2002       CHYCROTOCOTTANAACCAAACHTCACCAAACTTCACCACAACTTCACTTANAACTTCACAACAACTTACTT	
	PRIOR PRIOR SEQ ID TYPEST OREAN Duery M Best Lo Matchee	

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2418 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	Db       1340       AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAATTAACAGGGCCTCTCAC       1399       Oy         GY       61       TAACTAATCACTTTCCCATCTTTTGTTAGATTGAAATTAACATTCATGATCATTGCT       120       Oy         Db       1400       TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT       1459       Oy         Db       1400       TAACTAATCACTTTCCCATCTTTTGTTAGATTGAATTGA
TAATAATAATAATGCTAACAGAAAGAAAGAAAGGAACCGTTCGTT	Query Match     80.6%; Score 1376.6; DB 8; Length 2728;     Qy       Best Local Similarity     99.8%; Pred. No. 0;     Db       Matches 1388; Conservative     1; Mismatches     0; Indels     2; Gaps     1;       Qy     1 AATGAAAGATGAATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60     Qy     1
	y NAME/KEY: misc_feature
901 AGAGCTTGTATGGTTATGGACGTCTGACTAGGCATGÅTTTCACGAAGGCAAGATTGGCAT 960 	ŕ
841 TATGCGTGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA 900 	22 CURRENT FILING DATE: 2003-12-22 23 NUMBER OF SEC ID NOS: 73997 24 SOFTWARE: FastSEQ for Windows Version 4.0 25 SEC ID NO 3 26 SEC ID NO 3
781 ATATATATATATATATATATATAAAATATATATATATA	TITLE OF INVENTION: GENETIC TITLE OF INVENTION: GENETIC FILE REFERENCE: CLOO1499 CURRENT APPLICATION NUMBER:
721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	2 Sequence 3, Application US/10741600 2 Publication No. US20050026169A1 2 GENERAL INFORMATION: 2 ADPLICANT: CARGILL Michele of al DD
661 CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCAGAACATAGGGA 720 	ώ
601 CATGGTCGTTRAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGATTATA 660 	OY     1381 TTCTGGTTCAT 1391     OY       b     1 1 1 1 1 1     Db       b     2763 TTCTGGTTCAT 2773     Db
	OY       1321 CTTCTAGAGAGTTGCTGACCAACTGACGTATGTTTCCCTTTGTGAATTAATAAACTGGTG       1380       OY         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
	QY       1261 TITCTGGTTTCGTGTTCACCATGGAACATTTGATTATAGTTAATCCTTCTATCTTGAAT 1320       QY         Db       2643 TITCTGGTTTCGTGTTCACCATGGAACATTTGATTATAGTTAATCCTTCTATCTTGAAT 2702       Db
TCTATCA CAAGGCCAGTACCACACACTCATGAAGAAGAAGAACACGAGAGTAGCTGAGAGGCTA 	Oy         1201         GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT         1260         OY           Db         2583         GAGAAGGGTGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT         2642         Db
TCTCCAACCAAACATCAATGATTATTAGTTCTGTATACAGTACAGGACTTTGGTCTAC 	AACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG 1200
CAACTAACTCACTCAATTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCCTTGCT 	Qy         1081         CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG
CAAAATIGTGAAGTTAAATICTCCACTCTGTCCATCAGATACTATGGTICTCCACTATGG 	OY         1021         TAATAATAATGCTAACAGAAAGAGAAGAGAAACCGTTCGTT
CACTARAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGCCCAGCCCTTGA 	Oy         961         ATCATTGTAACTAAAAAAGCTGACATGACCAGACATATTGTACTCTTTCTAAAAATAA         1020         Oy         9           Db         2345         ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAATAA         2402         Db         Db         Db         2345         ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAATAA         2402         Db         Db         Db         Db         Db         Db         Db         DD         D
121 1460	Oy       901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT       Qy         Oy

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Oy       361       TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC       420         Db       1743       TCTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGACTCTTTGGTCTAC       1802         Oy       421       TCTATCACAAGGCCAGTACCACACTCATGAAGAAACACAGAACACAGGAGTAGCTGAGAGGCTA       480	IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	181 1563	Db 1443 TAACTAATCACTITICICITTIGITTAGATTIGAATATAAAATTCATGATCATGATCATGCT 1502 Oy 121 TTTTCTCTTTACAGGGGGAAATTTCATATTTTACCTGAGGAAATTGATTAGAAAATGGAA 180 	Qy       1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60         Db       1383 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAAATTAACAGGGCCTCTCAC 1442         Qy       61 TAACTAATCACTTTCCCAACGTTTTGTTAGATTGAAATTTAACAAGTACATGGATTGCT         Qy       61 TAACTAATCACTTTCCCAACGTTTTGTTAGATTGAAATTGAAAATTTAACAAGGCCTCTCAC 1442	M B Q	SE	; CURRENT APPLICATION NUMBER: US/10/741,600 ; CURRENT FILING DATE: 2003-12-22 ; NUMBER OF SEQ ID NOS: 73997 ; SOFTMARE: FastSEQ for Windows Version 4.0	APPLICANT: CARGILL, Michele et al. TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOOL499	6	Db 2718 TTCTGGTTCAT 2728 RESULT 14	1381 TICTGGTICAT 1391	1321 CTTCTAGAGAGTTGCTGACCTAACTGACGTATGTTTCCCTTTGTGAATTAATAACTGGTG 1321	DS 2598 THTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTCTATCTTGAAAT 1320	Db 2538 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTAAGTTGTCCT 2597	· ·
RESULT 15 US-10-741-600-2 ; Sequence 2, Application US/10741600 ; Publication No. US20050026169A1 ; GENERAL INFORMATION: ; APPLICANT: CARGILL, Michele et al.		IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1201 2581		100 246 114	$\begin{array}{llllllllllllllllllllllllllllllllllll$	Oy         841         TATGCGTGTGTGTAGACACAGGCATACACACATATAATGGAAGCAATAAGCCATTCTA         900           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		$\begin{array}{llllllllllllllllllllllllllllllllllll$	$\begin{array}{llllllllllllllllllllllllllllllllllll$	QY 601 CATGGTCGTTAAAGGAGAGATGGGGAGGATCATTCTGTTATACTTCTGTACACAGTTATA *** -		1863	Db 1803 TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACACAGGAGTAGCTGAGAGGGCTA 1862 Ov 481 AAACTCATCAAAAACACTACTCCTITTCCTCTACCCTATTCCTCAAACTTTTACCTTTTC 540	

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Qy         661         CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCAGAACATAGGGA         720           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy       601       CATGGTCGTTAAAGGAGAGAGAGGGGGAGCATCATTCTGTATACTTCTGTACACAGTTATA       660         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy         541         CANATCCCANTCCCCANATCAGTTITITCTCTTICTTACTCCCTCTCTCCCCTTTACCCTC         600	Oy       481 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540	Qy         421         TCTATCACAAGGCCAGTACCACACACTCATGAAGAACAACAGGAGTAGCTGAGAGGCTA         480	Qy       361       TCTCCAACCAAAACATCAATGTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC       420         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         301         CAACTAACTCACTCAATTTCCCTCCTAGCAGCATTCCATCTTCCCGATCTTCTTGCT         360           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         241         CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG         300	Oy         181 CCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCCCAGCCCTTGA 240	Qy         121 TITTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAGAAAATGGAA 180	Oy         61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATAT	Qy         1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60	Query Match80.6%;Score 1376.6;DB 8;Length 2777;Best Local Similarity99.8%;Pred. No. 0;Matches 1388;Conservative1;Matches 1388;Conservative1;	<pre>NAME_KEY: misc_feature NAME_KEY: misc_feature LOCATION: (1)(2777) OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1- US-10-741-600-2</pre>	រទ្ធម្ន	20	; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF ; FILE REFERENCE: CLOO1499 ; CURRENT APPLICATION NUMBER: US/10/741,600	
					Search completed: April 18, 2006, 13:17:15 Job time : 1704.66 secs	Db 2767 TTCTGGTTCAT 2777	2707	2647	1261	1141 2527 1901	1001 2467 1141	1021 2407		Qy 901 AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCA 	Qy 841 TATGCGTGTGTGTGTGTAGACACACACGCATACACACA 	Qy 781 ATATATATATATATATATATATATATATATATATATAT	•

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CTCCTTTAACTAGCATACCCCGAAGTG 1200 ngacatattgtactctttctaaaaataa 1020 |||||||||||||||||||||||||||| ngacatattgtactctttctaaaaataa 2406 2286 840 2226

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1       1701.8       99.7       305911       US-11-129-861-3       Sequence 3, Appli         1       1701.8       1272       14.5       1272       11       US-11-129-861-3       Sequence 3, Appli         1       1271.4       74.5       1273       11       US-11-129-861-76       Sequence 76, Appli         1       1260.8       74.4       1273       11       US-11-129-861-76       Sequence 77, Appl         1       1266.6       74.4       1273       11       US-11-129-861-76       Sequence 77, Appl         1       1260       73.8       1275       11       US-11-129-861-80       Sequence 78, Appl         1       1260       73.8       1275       11       US-11-129-861-80       Sequence 78, Appl         1       1260       73.8       1276       11       US-11-129-861-80       Sequence 82, Appl         11       127       60.2       1400       14       US-11-129-861-3654       Sequence 82, Appl         13       1027       60.2       2458       14       US-11-128-061-3654       Sequence 82, Appl         14       1027       60.2       2458       14       US-11-128-061-3654       Sequence 12, Appl         15       229.8 </th <th>SUMMARIES Y Description h Length DB ID Description</th> <th><pre>10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seqd:* 11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US61_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US61_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US61_NEW_PUB.seqd:* acore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.</pre></th> <th>Database : Published Applications NA_New:* 1: /SIDSS/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 2: /SIDSS/ptodata/2/pubpna/USO7_NEW_PUB.seq:* 4: /SIDSS/ptodata/2/pubpna/USO7_NEW_PUB.seq:* 5: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 6: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 8: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 8: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2:*</th> <th>Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries</th> <th>Total number of fits satisfying chosen parameters. Totatto Minimum DB seq length: 0 Maximum DB seq length: 2000000000</th> <th>Gapop 10.0 , Gapext 1.0 1: 9281099</th> <th>Title: US-09-884-901A-7 Perfect score: 1707 Sequence: 1 aatgaaagatggatttccaaggagtttcaggccaagctta 1707 Scoring table: IDENTITY_NUC</th> <th>OM nucleic - nucleic gearch, using sw model Run on: April 18, 2006, 12:50:18 ; Search time 1048.42 Seconds (without alignments) 6557.999 Million cell updates/sec</th> <th>GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.</th>	SUMMARIES Y Description h Length DB ID Description	<pre>10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seqd:* 11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US61_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US61_NEW_PUB.seqd:* 15: /SIDS5/ptodata/2/pubpna/US61_NEW_PUB.seqd:* acore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.</pre>	Database : Published Applications NA_New:* 1: /SIDSS/ptodata/2/pubpna/USO8_NEW_PUB.seq:* 2: /SIDSS/ptodata/2/pubpna/USO7_NEW_PUB.seq:* 4: /SIDSS/ptodata/2/pubpna/USO7_NEW_PUB.seq:* 5: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 6: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 8: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 8: /SIDSS/ptodata/2/pubpna/USO9_NEW_PUB.seq:* 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2:*	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Total number of fits satisfying chosen parameters. Totatto Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Gapop 10.0 , Gapext 1.0 1: 9281099	Title: US-09-884-901A-7 Perfect score: 1707 Sequence: 1 aatgaaagatggatttccaaggagtttcaggccaagctta 1707 Scoring table: IDENTITY_NUC	OM nucleic - nucleic gearch, using sw model Run on: April 18, 2006, 12:50:18 ; Search time 1048.42 Seconds (without alignments) 6557.999 Million cell updates/sec	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
OY       1       AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC       60         Db       34333       AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC       60         OY       1       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	JNA SM: Homo sapien: .861-4 .tch	9,861 925	ALIGNMENTS RESULT 1 US-11-129-861-4 ; Sequence 4, Application US/11129861 ; Publication No. US20060031956A1 ; GENERAL INFORMATION: ; APPLICANT: Kurachi, Kotoku ; APPLICANT: Kurachi, Sunicko ; APPLICANT: Kurachi, Sunicko	4 83.8 4.9 521 1 5 83.8 4.9 521 1	40 84 4.9 1047 10 US-10-301-480-651964 41 84 4.9 1047 10 US-10-301-480-651965 42 84 4.9 1047 10 US-10-301-480-651966 43 83.8 4.9 511 6 US-09-925-065A-344879	84 4.9 1047 9 US-10-301-480-38556 84 4.9 1047 9 US-10-301-480-38557 84 4.9 1047 10 US-10-301-480-651962 84 4.9 1047 10 US-10-301-480-651963 84 4.9 1047 10 US-10-301-480-651963	30         84.2         4.9         856         10         US-10-301-480-5196208           31         84         4.9         999         10         US-10-301-480-5196208           32         84         4.9         999         10         US-10-301-480-5196393           33         84         4.9         1047         9         US-10-301-480-38553           34         84         4.9         1047         9         US-10-301-480-38553           34         84         4.9         1047         9         US-10-301-480-38553           34         84         4.9         1047         9         US-10-301-480-38553	c       24       86       5.0       531       9       US-10-301-480-201172       Sequence 201172,         c       25       86       5.0       531       10       US-10-301-480-814581       Sequence 814581,         c       25       84       4.9       142605       14       US-11-121-086-64       Sequence 814581,         27       84.2       4.9       849       10       US-10-301-480-582800       Sequence 582800,         28       84.2       4.9       849       10       US-10-301-480-582800       Sequence 1196209,         28       84.2       4.9       849       10       US-10-301-480-582799       Sequence 1196209,         29       84.2       4.9       856       10       US-10-301-480-582799       Sequence 582799,         29       84.2       4.9       856       10       US-10-301-480-582799       Sequence 582799,         29       84.2       4.9       856       10       US-10-301-480-582799       Sequence 1196209,         29       84.2       4.9       856       10       US-10-301-480-582799,       Sequence 196279,	19 86.4 5.1 555 6 US-09-925-065A-308075 20 86.4 5.1 1758 6 US-09-925-065A-58792 21 86.4 5.1 1758 10 US-10-301-480-76030 22 86.4 5.1 1758 10 US-10-301-480-773439 23 86 5.0 528 6 US-09-925-065A-100582

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291	35593 TTTCTGGTTTCGTGTTCACCATGGAACATTTGATTATAGTTAATCCTTCTATCTTGAAT	_
Db 181 CAGCCCTTGACAAAATTGTGAAGTTA	Db 35533 GAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATCCCAATCAGCCAACTAAGTTGTCCT 35592 Oy 1261 TTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTAAGTTAATCCTTCTATCTTGAAT 1320	<b>_</b> .
121		_
Db 61 GATCAITGCTTTTTTCTCTTTACAGe Oy 171 GAAAATGGAACCACTAGAGGAATATA 	Oy         1141         AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG         1200           Db         35473         AGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATACCCCGAAGTG         35532	
	35413 (TTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCAAG	
Db 1 GGCCTCTCACTAATAATCACTTTCC	D5 35353 TAATAATAATACAGAAAGAAGAAGAAACCGTTCGTTTGCAATCTACAGCTAGTAGAGA 35412 OY 1081 CTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGGCCAAGCAAG	_
Best Local Similarity 100.0%; pred Matches 1273; Conservative 0; Mit	Oy         1021         ТААТААТААТССТААСАЗАЛАЗАЗАЗАЗАЗАССТТОСТТИССААТСТАСАЗСТАЗАТАЗАЗА         1080	
9-861-3 Match 74.6%; \$	Qy         961         ATCATTGTAACTAAAAAAGCTGACATTGACCCGAGACATATTGTACTCTTTCTAAAAATAA         1020           Qy	
; SEQ ID NO 3 ; LENGTH: 1273 ; TYPE: DNA 27 ; ORGANISM: Homo sabiens	QY         901         AGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT         960           Db         35233         AGAGCTTGTATGGTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCAAGATTGGCAT         35292	
; PRIOR APPLICATION NUMBER: US/09/328, ; PRIOR FILING DATE: 1999-06-09 ; NUMBER OF SEQ ID NOS: 84 ; SOFTWARE: Patentin Ver. 2.0	Oy         841         TATEGETGTETAGACACACACECTATACACECTATATEGEAACAATAAGCOATTCTA         900           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
; TITLE OF INVENTION: USe Thereot ; FILE REPERENCE: UM-03603 ; CURRENT APPLICATION NUMBER: US/11/12; ; CURRENT FILING DATE: 2005-05-16	781 ATATATATAATAATAATAATAATAATAATAATAATAAAATAAAA	
; GENERAL INFORMATION: ; APPLICANT: Kurachi, Kotoku ; APPLICANT: Kurachi, Sumiko ; TITLE OF INVENTION: Nucleotide Sequei	721 35053	
RESULT 2 US-11-129-861-3 ; Sequence 3, Application US/11129861 ; Publication No. US20060031956A1	OY         661         CATGICIATCAAACCCAGACTTGCTTCCATAGIGGAGACTTGCTTTTCAGAACATAGGGA         720           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
. 36013	Qy         601         CATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA         660	
ω	Qy         541         CANATCECANTCECCANATCAGETTITETETTETTETTETTETETETETECECTETTECECTTTACCCCC         600           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
35893	Oy         481         Amactcatcamamacactactcctittcctctaccctattcctcaatcttttaccttttaccttttc         540           01         111111111111111111111111111111111111	
35833	Qy         421         TCTATCACAAGGCCAGTACCACACTCATGAAGAAAGAACAACAGGAGTAGCTCAGAGGGCTA         480	
Db 35773 TGATGATGATGAGGACTACTGACAA	Qy 361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420 	
35713	QY       301       CAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT       360         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
Db 1381 TICIGGTICATACCTIGGCTITITG	Oy 241 CAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTCTCCACTATGG 300 	
1001		

re 1273; DB 11; Length 1273; rd. No. 1.8e-61; fismatches 0; Indels 0; , 925 29,861 ences for Gene Regulation and Methods of T 1705 AAATCACTCTGACCCTGCCAAGCTGCCTGCCTTCTCC 1500 AATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350 GGAGAATTTCATATTTACCTGAGCAAATTGATTA 120 3GGAGAATTTCATATTTTACCTGAGCAAATTGATTA 170 **т** 36037 GCCTCACTCTTGCTAGTTCCTTTAGTC 35892 GCCTCACTCTTGCTAGTTCCTTTAGTCCTTTAGTC 1560 Indels 0; Gaps 240 290 0

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RESULT 3 US-11-129-	р 8	8 Q	Qу Db	p Q	р 9 У 4	5 g	р 92	da Að	P Q	V	р Q	в <i>б</i>	\$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$ \$
3 129-861-83	1311 TATCTTGAATCTT 1323                 1261 TATCTTGAATCTT 1273	1251 AAGTTGTCCTTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC 1310 	1191 CCCCGAAGTGGAGAAGGGTGCAAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT 1250 	1131 AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA 1190 	1071         CTAGTAGAGAGTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC         1130	1011 CTAAAAATAATAATAATAATGCTAACAGAAAGAAAGAAGAAGAACCGTTCGTT	951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010 	891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950 	831 TGTGTGTGTGTGTATGCGTGTGTGTAGACACACACACACA	771 AAGTTATTTTATATATATAATATATATATATAAAAAAAA	711 AACATAGGGATGAAGTAAGGTCCCTGAAAAGTTTGGGGGAAAAGTTTCTTCAGAGAGTT 770 	651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710 	241 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTCAGCAGCATTCCATCTTCCCGAT 300 351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410 301 CTTCTTTGCTTACTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 360 411 TTTGGTCTACTCATCAAAGGCCAGTACCACACTCATGAAAGAAA
Oy         712         ACATAGGGATGAAGTAAGGTGCCTCAAAAGTTTGGGGGAAAAGTTTCTTTC	QY         652         ACAGTTATACATGTCTATCAAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCAGA         711           Db         601         ACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCAGA         660			n 4	Oy         412         TIGGTCTACTCTATCACAAGGCCAGTACCACACCATGAAGAAAGA		QY         292         CCACTATGGCAACTAACTCAACTCAATTTTCCCTCCTAGCAGCATTCCATCTTCCCGATC         351           Db         241         CCACTATGGCAACTCAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCCGATC         300		QY         172         AAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGCCCC         231	Qy         112 ATCATTGCTTTTTCTCTTTACAGGGGGGAGAATTTCATATTTACCTGAGCAAATTGATTAG         171           Db         61 ATCATTGCTTTTTCTCTTTACAGGGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAG         120	Oy         52         GCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATACATTCTATG         111           Db         1 <td></td> <td><pre>Sequence 83, Application US/11129861 Publication No. US20060031956A1 GENERAL INFORMATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Sumiko TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of TITLE OF INVENTION: Use Thereof FILE REFERENCE: UN-03603 CURRENT FILING DATE: 2005-05-16 PRIOR APPLICATION NUMBER: US/11/129,861 CURRENT FILING DATE: 2005-05-16 PRIOR APPLICATION NUMBER: US/11/129,861 SOFTWARE: PatentIn Ver0503 INVESE OF SEQ ID NOS: 84 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 83 LENGTH: 1272 TYPE: DNA CORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-11-129-861-83</pre></td>		<pre>Sequence 83, Application US/11129861 Publication No. US20060031956A1 GENERAL INFORMATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Sumiko TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of TITLE OF INVENTION: Use Thereof FILE REFERENCE: UN-03603 CURRENT FILING DATE: 2005-05-16 PRIOR APPLICATION NUMBER: US/11/129,861 CURRENT FILING DATE: 2005-05-16 PRIOR APPLICATION NUMBER: US/11/129,861 SOFTWARE: PatentIn Ver0503 INVESE OF SEQ ID NOS: 84 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 83 LENGTH: 1272 TYPE: DNA CORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-11-129-861-83</pre>

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1071 CTAGTAGAGACTFTGAGAAGAATTCAAACAGTGTGTCTTCAGAGTGTTCAGAGGCCAAGC 	<u> </u>	Query Match       74.5%; Score 1271.4; DB 11; Length 1273;         Best Local Similarity       99.9%; Pred. No. 2.2e-61;         Matches 1272; Conservative       0; Mismatches         Qy       51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATAT
сталалатлатаатаатаатастаасадаладаадаадаассдттсдттдслатстасад 	da Að	S-1
951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCCAGACATATTGTACTCTTT 1010 	da Að	SOFTWARE PATENTIN VET. 2.0 SEQ ID NO 76 LENGTH: 1273
891 AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA 950 	QY	CONNERT FILING DATE: 2005-05-16/16/10/ FRIOR APPLICATION NUMBER: US/09/328,925 FRIOR FILING DATE: 1999-06-09
831 TGTGTGTGTGTGTATGCGTGTGTGTAGACACACACACACA	QY	° 7
771 AAGTTATTTATATATATATATATATATATATAAAATATATAATAT	DP QY	APPLICATION NO. US2000 GENERAL INFORMATION: APPLICANT: Kurachi, I
711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	DP DP	ESULT 4 S-11-129-861-
651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710 	da Võ	Oy         1312 ATCTTGAATCTT 1323           Db         1261 ATCTTGAATCTT 1272
591 TITITACCCTCCATGGTCGTTAAAGGAGAGAGAGGAGGAGCATCATTCTGTTATACTTCTGTA 650 	D QY	Oy         1252         AGTIGICCTITICIGGITICGIGITICACCATGGAACATITIGATATAGTTAATACTTCI 1311           Db         1201         AGTIGICCTITICIGGITICGIGITICACCATGGAACATITIGATIATAGTTAATACTTCI 1260
531 TTACCTTTTCCAAATCCCAATCCCCAAATCAGTTTTTTCTCTTTTCTTACTCCCCTCTCTCCC 590	DB QY	Oy         1192         CCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACTA         1251           Db
471 TGAGAGGCTAAAACTCATGAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT 530 	Å Å	Qy         1132         AGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATAC         1191           Db
411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGA	DP DP	Qy         1072         TAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGCCAAGCA         1131           .
351       CTTCTTTGCTTCTCCAACCAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC       410	ab Vy	Qy         1012         талалатлаталталталтастасадаласадаласадалссоттсоттгосалтстасадс         1071           Qy
291 TCCACTATGGCAACTAACTCAACTCAATTTTCCCTCCTAGCAGCATTCCATCTTCCCGAT 350 	dg Qy	Oy         952         GATTGGCATATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTC         1011           01
231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCACTCTGTCCATCAGATACTATGGTTC 290 	DP CA	Qy         892         GCCATTCTAAGAGCTTGTATGGTATGGTCTGACCTAGCATGATTTCACGAAGGCAA         951
171         GAAAATGGAACCACTAGAGGAATATAAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC         230	. DP	Oy         832         GTGTGTGTGTGTATGCGTGTGTGTAGACACACACACACAC
111 GATCATTGCTTTTCTCTTTACAGGGGGGAGAATTTCATATTTACCTGAGCAAATTGATTA         170	DP QX	0y 772 agttatttatatatatatatatatatatatatatatata
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Sequence 77, Application US/11129861 Sequence 77, Application US/11129861 Bublication No. US20060031956A1 GENERAL INFORMATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Sumiko TITLE OF INVENTION: Use Thereof FILS REFERENCE: UM-03603 CURRENT APPLICATION NUMBER: US/11/129,861 CURRENT APPLICATION NUMBER: US/01/129,861 CURRENT APPLICATION NUMBER: US/09/328,925 PRIOR APPLICATION NUMBER: US/09/328,925 PRIOR FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 84 SOFTWARE: PatentIN Ver. 2.0 SEQ ID NO 77 LEBUTH: 1273 TYPE: DNA CORGANISM: Artificial Sequence Ş 몋 Ş 망 Ş 昂 ą 昂 Ş 뭥 Ş 昂 Ş 뭥 Ś ş B Ş 昂 ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: US-11-129-861-77 RESULT 5 US-11-129-861-77 Ş 昂 昂 Query Match Best Local Simi Matches 1272; Local Similarity 1311 1201 1251 1141 1191 1261 301 181 421 471 361 411 351 241 291 231 121 171 111 13 51 ч CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTC CAGCCCTTGACAAAATTGTGAAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTC 290 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC TATCTTGAATCTT 1273 TATCTTGAATCTT CCCCGAAGTGGAGAAGGGTGCAGGCAGGCTCAAAGGCATAAGTCATTCCCAATCAGCCAACT CCCCGAAGTGGAGAAGGGTGCAGGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT TGAGAGGCTAAAAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCCTATTCCTCAATCTT 530 **CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC** TCCACTATOGCAACTAACTCACTCAAATTTCCCTCCTTAGCAGCATTCCCATCTTCCCGAT Conservative 74.5**%;** 99.9**%;** 1323 °, Score 1271.4; DB 11; Pred. No. 2.2e-61; 0; Mismatches 1; I Indels Length Synthetic and 1273; °, Methods Gaps 410 350 470 300 1200 1250 360 240 180 230 420 ĉ 0 RESULT 6 US-11-129-861-78 Sequence 78, Application US/11129861 Publication No. US20060031956A1 GENERAL INFORMATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Kotoku TITLE OF INVENTION: Use Thereof FILE REFERENCE: UM-03603 CURRENT APPLICATION NUMBER: US/11/129,861 CURRENT APPLICATION NUMBER: US/11/129,861 CURRENT APPLICATION NUMBER: US/09/328,925 PRIOR APPLICATION NUMBER: US/09/328,925 NUMBER OF SEC ID NOS: 84 片 Ş 昂 Ş B Ş 문 Ş 뭥 Ş 망 ş 昂 Ś 昂 Ş 뭥 ą 昂 Ş 昂 Ş 뭉 Ş 뭥 Ş 뎡 Ş SOFTWARE : 1261 1311 1201 1141 1191 1081 1131 1021 1251 1071 1011 196 901 951 841 168 831 661 601 651 541 591 481 531 781 721 771 711 PatentIn TATCTTGAATCTT 1273 TATCTTGAATCTT AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCCTTTAACTAGCATA CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGGCCAAGC CTAAAAATAATAATAATAATGCTAACAGAAAGAAGAACGGTTCGTTTGCAATCTACAG AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA AGCCATTCTAAGAGCTTCTATGGTTATGGAGGGCTTGACTAGGCATGATTTCACGAAGGCA CACAGTTATACATGTCTATCAAAACCCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG AAGITGTCCTTTTTCGGGTTTCGTGTTCACCATGGAACATTTGATTATAGTTAAATCCTTC 1310 TGTGTGTGTGTGTGTGTGTGTGTGTGGACACACGCATACACACATATAATGGAAGCAATA AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA Ver. N 1323 • for Gene Regulation and Methods 1190 1010 1250 1140 900 840 068 600 650 540 1260 1200 1080 1130 1020 1070 960 950 780 830 770 099 590 720 710 e f

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QY       891       AGCCATTCTAAGAGCTTGTATGGATGTGACTAGGCATGATTTCACGAAGGCA       950         Db       841       AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA       900         . QY       951       AGATTGGCATATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT       1010	Qy 831 TGTGTGTGTGTGTATGCGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATA 890 	0y 771 aagttatttatatatatatatatatatatatatatatat	Qy         711         Aacatagggatgaagtaagtaggtgcctgaaaagttcggggaaaagtttctttc	Qy       < 651       CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG       710         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         591         TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTGTA         650	QY       531 TTACCTTTTCCAAATCCCCAAATCCCCAAATCAGTTTTTCTCTTTCTT	Oy         471         TEAGAGGCTAAAACTCATCATCAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT         530           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGA	Qy         351         CTTCTTTCCTTCCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC         410           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy       291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCGAT 350	Oy         231         CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTC         290	Oy         171         Gaaaatggaaccactagaggaatataatgtgttaggaaattacagtcatttctaacggcc         230           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy         111         GATCATTGCTTTTTCTCTTTACAGGGGAGAATTTCATATTTACCTGAGCAAATTGATTA         170           0	Oy         51         GGCCTCTCACTAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATAT	Query Match 74.4%; Score 1269.8; DB 11; Length 1273; Best Local Similarity 99.8%; Pred. No. 2.7e-61; Matches 1271; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	; IIF5: UNA ; ORGANISM: Artificial Sequence ; PEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-11-129-861-78	; SEQ ID NO 78 ; LENGTH: 1273
Qy       231       CAGECCETTGACAAAATTGTGAAGTTAAATTETECCACTCTGTECATCAGATACGETTC       290         Db       181       CAGECCETTGACAAAATTGTGAAGTTAAATTETECCACTCTGTECAATCAGATACTATGGTTC       240         Qy       291       TECACTATGGCAACTAACTCACTCAATTTECECCTCTTAGCAGCATTECCATCCAATCATCTECCGAT       350	Oy         171         GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC         230		OY       \$1       GCCTCTCACTAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATACATTCTAT       110         Db       1       GCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTAT, 60	Query Match 74.2%; Score 1266.6; DB 11; Length 1273; Best Local Similarity 99.7%; Pred. No. 4e-61; Matches 1269; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		ñ	PRIOR APPLICATION NUMBER: US/09/328,925 PRIOR FILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 84 SOPTWARE: FACENTIN VET. 2.0	nereof : US/11/129,861 .05-16	INFORMATION: NT: Kurachi, NT: Kurachi,	RESULT 7 US-11-129-861-79 / Sequence 79, Application US/11129861 - Dublication No. US20060031956A1	Db 1261 TATCTTGAATCTT 1273	1201 AAGTEGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC	1251 CCCCCGAAGTGGAGAAAGGGTGCAGGAGCACCATGGAACATTAAGTCAATCAGCCTAATCAGCCTAACCT	1081 AAGAAGTTGAAGTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA	1071 1021	1011 сталалаталталталталтастолсадаладаладададасстотстотостотосаластасад 	Db 901 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 960

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RESULT	DP QA	DP Q	р 25	р р	DP QA	DP QY	DP QY	DP QV	DP QY	8 8	p Q	5 5 2	DP Q	dp Qy	B &	B &	DB QY	др
α.	1311 TATCTTGAATCTT 1323                   1261 TATCTTGAATCTT 1273	1251       AAGTIGTCCTTITICTGGTTTCGTGTTCGACCATGGAACATTTTGATTATAGTTAATCCTTC       1310	1191         CCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT         1250	1131       AAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCATA       1190	1071 CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTGTCTTCAGCAGTGTTCAGAGCCAAGC 1130 	1011 CTAAAAAATAATAATAATAATGCTAACAGAAAGAAAGAGAGAG	951 AGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTT 1010 	891         AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA         950	831 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGACACACACA	771 AAGTTATTTTATATATATATATATATATATAAAATATATAATAT	711         AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAG 710 	591         TTTTACCCTCCATGGTCGTTAAAGGAGAGAATGGGGAGCATCATTCTGTTATACTTCTGTA         650	531 TTACCTTTTCCAAATCCCCAAATCCCCAAATCAGTTTTTCTCTTTTCTTACTCCCCTCTCTCCC 590	471         TGAGAGGCTAAAAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTT         530	411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGA	351 CTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATC 410 	
					<b>.</b>											·		
Q	AC 40	Qy da	Qy Db	5 Q	da Ad	DP QA	Ad Ad	dg Qy	da VQ	Ad Ad	QY dd	Query I Best Lo Matche	; FEAT ; OTHE US-11-12	SEQ ID	PRIOR A PRIOR F NUMBER SOFTWAR	; TITLE O ; FILE RE ; CURRENT	; GENERAL ; APPLIC ; APPLIC ; TITLE	US-11-12; ; Sequence; ; Public;
711 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	651 CACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATACTGGAGACTTGCTTTCAG 710 	<ul> <li>591 TTTTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATCTGTTATACTCTGTA 650</li> <li>                                    </li></ul>			411 TTTGGTCTACTCTATCACAAGGCCAGTACCACACACTCATGAAGAAAGA		291 TCCACTATGGCAACTAACTCAACTCAATTTTCCCTCCTAGCAGCATTCCATCTTCCCGAT 350 			111         GATCATTGCTTTTTTTTTTTTTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA         170	51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATAT	Query Match 73.9%; Score 1261; DB 11; Length 1272; Best Local Similarity 99.9%; Pred. No. 8e-61; Matches 1272; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic -11-129-861-82	NO 8 ITH: 1 IDNA: NISM:	APPLICATION NUMBER: US/09/328,925 FILING DATE: 1999-06-09 R OF SEQ ID NOS: 84 ARE: Pacentin Ver. 2.0	/129,861	GEMEKAL INFORMATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Sumiko TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of	-11-129-861-82 Sequence 82, Application US/11129861 Publication No. US20060031956A1

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1129 GCAAGAAGTTGAAGTTGCCTAGACCAGAGGACATAAGTATCATGTCTCCTTTAACTAGCA	Q	Matches 1273; Conservative 0; Mismatches 0; Indels 2; Gaps 1; Ov 51 GGCCTCTCACTAACTAATCACTTTCCCATCTTTGTTAGATTTGAATATATACATTCTAT 110
1069 AGCTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGGCCAA 	QY	uery Match 73.9%; Score 1261; DB 11; Length 1275; est Local Similarity 99.8%; Pred. No. 8e-61;
1009 TTCTAAAAATAATAATAATAATGCTAACAGAAAGAAGAAGAACCGTTCGTT	AD AD	) ) ORGANISM: Artificial Sequence ; PEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-11-129-861-80
949 CAAGATTGGCATATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCT 	QY	; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 80 ; LENGTH: 1275
889 TAAGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGG 	DP QY	CURRENT FILING DATE: 2005-05-16 PRIOR APPLICATION NUMBER: US/09/328,925 PRIOR FILING DATE: 1999-06-09 NUMBER OF SEO ID NOS: 84
829 AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTAGACACACGCATACACACATATAATGGAAGCAA 	dg VQ	<pre>i TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of i TITLE OF INVENTION: Use Thereof i FILE REFERENCE: UM-03603 i CURRENT APPLICATION NUMBER: US/11/129 A61</pre>
769   TTAAGTTATTTTATATATATATATATATATATAAAATATATAATAT	Ad Vo	<pre>Publication No. US20060031956A1 ; Publication No. US20060031956A1 ; GENERAL INFORMATION: ; APPLICANT: Kurachi, Kotoku ; APPLICANT: Kurachi, Sumiko</pre>
709 AGAACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	8 8	RESULT 9 US-11-129-861-80 - Company 861-80
649 TACACAGTTATACATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTC 	Ad Ad	Qy         1311 TATCTTGAATCTT 1323           Db         1260 TATCTTGAATCTT 1272
589         CCTTFTACCCTCCATGGTCGTTAAAGGAGAGATGGGGAGCATCATTCTGTTATACTTCTG	A V	Qy         1251         AAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCTTC         1310           Db
529 TTTACCTTTTCCAAATCCCAATCCCCAAACAGTTTTTCTCTTTCTT	Ad Ad	Qy         1191         CCCCGAAGTGGAGAAGGGTGCAGGAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAACT         1250           Db
469         GCTGAGAGGCTAAAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATG	DB QY	Qy         1131         Angaagttgaagttgcctagaccagaggacataagtatcatgtctcctttaactaagcata         1190           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
409         TCTTTGGTCTACTCTATCACAAGGCCAGTACCACACTCATGAAGAAAGA	4a VO	Qy         1071         CTAGTAGAGACTTTGAGGAAGAATTCAACAGTGTGTCTTCAGCAGTGTTCAGAGGCCAAGC         1130           Db
350 - TCTTCTTTGCTTCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGA 	da Qy	Qy         1011         сталалатаатаатаатаатастаасадаладаадаадаадаадаассуттсуттусаатстасад         1070           U
291 TCCACTATGGCAACTAACTCACTCAATTTTCCCTCCTAGCAGCATTCCATCTTCCCGA- 	DP 63	Qy         951         AGATTGGCATATCATTGTAACTAAAAAAGCTGACCATGACCCCAGACATATTGTACTCTTT         1010           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
231 CAGCCCTTGACAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTC 	р <i>б</i>	Qy         891         AGCCATTCTAAGAGCTTGTATGGTTATGGAGGTCTGACTAGGCATGATTTCACGAAGGCA         950
171 GAAAATGGAACCACTAGAGGAATATAATGTGTTAGGAAATTACAGTCATTTCTAAGGGCC 	р <i>б</i>	Qy         831         TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGAGACACACAC
111 GATCATTCCTTTTTCTCTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTA 	D QY	Qy 771 AAGTTATTTATATATATATATATATATATATATAAAATATATA
1 GGCCTCTCACTAACTAATCACTTTCCCCATCTTTTGTTAGATTTGAATATATACATTCTAT	ממ	DD 661 AACATAGGGATGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC

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QY       291       TCCACTATGGCAACTAACTCACTCATTACCCTCCTTAGCAGCATTCCATCCTTAGCAGCATTCCATCCCCCAT       350         Db       241       TCCACTATGGCAACTAACTCACTCACTCAATTTTCCCTCCTTAGCAGCATTCCATCTTCCCCCAT       300         QY       351       CTTCTTTGCTTCTCCCAACTAACTCACTCACTCATTTTTCCCTCCTTAGCAGCATTCCATCTTCCCCAT       300         QY       351       CTTCTTTGCTTCTCCCAACCAAAACTCAACTCAATGTTTATTAGTTCTGTATACAGTACAGGATC       300         QY       301       CTTCTTTGGTTTCTCCCAACCAAAACTCAATGTTTATTAGTTCTGTATACAGTACAGGATC       360         QY       411       TTTGGTCTACTCTCTAACACAAAACTCAATGTTTATTAGTTCTGTATACAGGATAGGATAG       360         QY       411       TTTGGTCTACTCTCTATCACAAAGGCCAGTACCACACTCATGAAGAAAGA		<pre>RESULT 10 RESULT 10 Sequence 81, Application US/11129861 Publication No. US20060031956A1 GENERAL INFORMATION: APPLICANT: Kurachi, Kotoku APPLICANT: Kurachi, Sumiko TITLE OF INVERTION: Nuclectide Sequences for Gene Regulation and Methods of TITLE OF INVERTION: Use Thereof FILE REFERENCE: UM-03603 CURRENT FLILING DATE: 2006-05-16 FRIOR APPLICATION NUMBER: US/11/129,861 CURRENT FLILING DATE: 1999-06-09 NUMBER OF SEQ ID NOS: 84 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 81 LENGTH: 1276 TYPE: DNA CRGANISM: Artificial Sequence FEATURE: COTHER INFORMATION: Description of Artificial Sequence: Synthetic US-11-129-861-81</pre>	QY       1189       TACCCCGAAGTGGAGAAGGGTGCAGGAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAA       1248         Db       1141       TACCCCGAAGTGGAGAAGGGTGCAGCAGGCTCAAAGGCATAAGTCATTCCAATCAGCCAA       1200         QY       1249       CTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACAGTCATTCGATCATTCAATCCT       1308         Db       1201       CTAAGTTGTCCTTTTCTGGTTTCGTGTTCACCATGGAACATTTTGATTATAGTTAATCCT       1260         QY       1309       TCTAATCTTGAATCTT       1323         Db       1261       TCTAATCTTGAATCTT       1275
RESULT 11 RESULT 11 Sequence 3654, Application US/11128061 Publication No. US20060003958A1 GENERAL INFORMATION: APPLICANT: Melville, Mark W. APPLICANT: Mounts, William M. APPLICANT: Mounts, William M. APPLICANT: Hann, Louane E. APPLICANT: Sinacore, Martin S. APPLICANT: Sinacore, Martin S. APPLICANT: Brown, Eugene L. APPLICANT: Miller, Christopher P. TITLE OF INVENTION: NOVEL FOLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS TITLE OF INVENTION: TO MONITOR GENE EXPRESSION	Db       1021       CTAGTAGAGACTTTTGAGGAAGAATACAACAACAACAACAACAACAACAACAACAACAACAA	661 771 721 831 781 841 901 1011 1011	QY       531 TTACCTTTTCCAAATCCCAAATCAGTTTTTCTCTTTACTCCCTCTCCC       590         Db       481 TTACCTTTTCCAAATCCCAAATCCCAAATCAGTTTTTCTCTTTTTTTCTCTTTACTCCCTCTCCC       540         QY       591 TTTTACCCTTCCAATCCCCAAATCCCAAATCAGTTTTTCTCTTTTCTCTTTACTCCCTTCTCTC       540         Db       541 TTTTACCCTTCCAATGGTCGTTAAAGAAGAAGAAGAGAGGAGGAGCATCATTCTGTTATACTTCTGTA       600         QY       651 CACAGTTATACATGCTCTATCAAACCAGACTTGCTTCCCATAGTGGGAGACTTGCTTTTCAG       600         Db       601 CACAGTTATACATGTTATCAAACCAGACTTGCTTCCATAGTGGGAGACTTGCTTTTCAG       600         QY       711 AACATAGGGATGAAGTAAGTAAGTAAGTGCTGAAAAGTTTGGGGGAAAAAGTTTGCTTTCAAGAGATT       710         QY       711 AACATAGGGATGAAGTAAAGTAAGTGCTGAAAAGTTTGGGGGAAAAAGTTTGCTTTCAAGAGATT       601

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661       CATGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCAGAACATAGGGA         101       10	bb       781       fcfatchaddeccagfaccacctchreadectrodadechaddech	if TTRE:       Description         is:       Description         is:       11.128-061.3654         Description:       60.2%; Score 1027; DB 14; Length 1400; Best Local Similarity 100.0%; Pred. No. 2.8e-48; Indels 0; Gaps 0; Patches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;         QY       1       ANTGAMAGATGGATTICCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420         QY       1       ANTGAMAGATGGATTICCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420         QY       1       ANTGAMAGATGGATTICCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420         QY       1       ANTGAMAGATGGATTICCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420         QY       1       TAACCAAACGACTTCCCAATTCCAAGGTTAATTCAATTGAATTAACAGGGCCTCTCAC 420         QY       1       TAACCAAACGACGATTCCAAGGTTAATTCAATTGAATTAACAATTGAAAATTGAA         DD       40       TTTCCTCTTPACAGGGGAGATTTCAAATTAACATTGAAAATTGAA         DD       10       11       11         DD       12       TTTCCTCTTPACAGGGGAGAATTAACAGTCATTGCTAAGGGCCCAGGCCCTTGG       20         QY       13       TTTCCTCTTPACAGGGGAAATTAACGTCATTGCTAAGGGCCCAAGGCCCAGGCC	<pre># FILE REFERENCE: 01997.027701 # CURRENT APPLICATION NUMBER: US/11/128,061 # CURRENT FILING DATE: 2005-05-11 # PRIOR APPLICATION NUMBER: US 60/570,425 # PRIOR FILING DATE: 2004-05-11 # NUMBER OF SEQ ID NOS: 7285 # SOFTWARE: PatentIn version 3.3 # SEQ_ID NO 3654 # SEQ_ID NO 3654</pre>
181       CCACTAGAGGAATATAATGTGTTTAGGAAATTACAGTCATTTCTAAGGGCCCAGGCCCTTGA         181       CCACTAGAGGAATATAATGTGTTTAGGAAATTACAGTCATTTCTAAGGGCCCAGGCCCTTGA         241       CCACTAGAGGAATATAATGTGTTTAGGAAATTACAGTCATTACTATGGTTCTCCACTATGG         1111       1111         601       CAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCACTCAGATACTATGGTTCTCCCACTATGG         301       CAACTAACTCACTCAATTTCCCCCCTCCTTAGCAGCATTCCATCTATGGTTCTCCCGATCTTGCT         611       CAACTAACTCACTCAATTTTCCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCCTTGCT         661       CAACTAACTCACTCACTCAATTTCCCCTCCTTAGCAGCATTCCATCTTCCCGATCTTCTTTGCT	Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;         QY       1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60         Db       361 AATGAAAGATGGATTTCCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420         QY       61 TAACTAATCACTTTCCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 420         Db       421 TAACTAATCACTTTCCCAAGGTTAATTCATTGGAATTGAAATTAACATTCATGATCATTGCT 480         QY       121 TTTTCCTTTACACGTTTCCTTTGTTAGATTTGAATATATAAATTCAATGGAAATGGAAATGGAA         Db       421 TTTTCCTCTTTACACGTTTCCTTTGTTAGATTTGAATATATAACATTCTATGATCATTGCT         Db       421 TTTTCCTCTTTACACTTTCCATCTTTGTTAGATTTCAATATATAACATTCTATGATCATTGGAA         Db       421 TTTTCCTCTTTACACGGGGGGAGAATTTCATTTCATTTTTTTT	9 1 ALCATTGTAACTAAAAAAA 1 221 ATCATTGTAACTAAAAAAAA 1 221 ATCATTGTAACTAAAAAAAA 1 221 TAATAAT 1027 1 381 TAATAAT 1387 1 381 TAATAAT 1387 1 28 ence 3654, Application US/1: ence 3654, Application US/1: LICANT: Melville, Mark W. LICANT: Melville, Mark W. LICANT: Mounts, William M. LICANT: Leonard, Mark W. LICANT: Leonard, Mark W. LICANT: Brown, Eugene L. LICANT: Brown, Eugene L. LICANT: Brown, Christophei LICANT: Miller, Christophei LICANT: MILLER, Christophei LICANT: MILLER, Christophei LICANT: MILLER, Christophei LICANT: Brown NUMBER: US CO F INVENTION NUMBER: US CO F INVENTION NUMBER: US REFERENCE: 0197.027700 REFERENCE: 2004-05-11 BER OF SEQ ID NOS: 7285 TMARE: Patentin version 3.3 NGTH: 1400 PE: DNA 128-049-3654 128-049-365	841       TATEGGTGTGTGTGTAGACACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA

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APFLICANT: Sinacore, Martin S. APPLICANT: Leonard, Mark W. APPLICANT: Leonard, Mark W. APPLICANT: Leonard, Mark W. APPLICANT: Brown, Bugene L. APPLICANT: MILLE, Christeopher P. TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ( TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ( TURENT APPLICATION NUMBER: US/11/128,061 CURRENT APPLICATION NUMBER: US/11/128,061 CURRENT PILING DATE: 2005-05-11 PRIOR PILING DATE: 2004-05-11 NUMBER OF SEQ ID NOIS: 7205 SOFTWARE: Patentin version 3.3 SEQ ID NO 12 LENGTH: 2458	RESULT 13 US-11-128-061-12 Sequence 12, Application US/11128061 Fublication No. US20060003958A1 GENERAL INFORMATION: APPLICANT: Melville, Mark W. APPLICANT: Charlebois, Timothy S. APPLICANT: Charlebois, Timothy S.	Qy         961 ATCATTGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1020           Db         1321 ATCATTGTAACTAAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA 1380           Qy         1021 TAATAAT 1027           IIIIIIII           Db         1381 TAATAAT 1387		721       TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTCAGAGAGTTAAGTTATTTT         721       TGAAGTAAGGTGCCTGAAAAGTTTGGGGGAAAAGTTTCTTTC	QY       601       CATGGTCGTTAAAGGAGAGAGGGGAGCATCATTCTGTATAACTTCTGTACACACGTTATA       660         Db       961       CATGGTCGTTAAAGGAGAGAGGGGGAGCATCATTCTGTATAACTTCTGTACACACGTTATA       1020         QY       661       CATGGTCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA       720         QY       1021       CATGGTCTATCAAACCCAGACTTGCTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA       720         Dh       1021       CATGGTCTATCAAACCCCAGACTTGCTTGCTTCCATAGTGGAGACTTGCTTTTCAGAACATAGGGA       1080	QY       481 AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAARTCTTTTACCTTTTC       540         Db       841 AAACTCATCAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAARTCTTTTACCTTTTC       900         QY       541 CAAATCCCAATCCCCAARTCAGTTTTTCCTCTTTCTTACCCTCTCCCCCCTTTTACCCTTTACCCTC       600         Db       901 CAAATCCCAATCCCCAATCAGTTTTTCTCTTTCTTACTCCTCCCCTCTCCCCTTTTACCCTC       960	Qy       361 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 420         Db       721 TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 780         Qy       421 TCTATCACAAGGCCAGTACCACACTCAATGTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC 780         Db       781 TCTATCACAAGGCCAGTACCACACTCAATGAAGAAAGAACACAGGAGTAGCTGAGAGGCTA 840         Db       781 TCTATCACAAGGCCAGTACCACACTCAATGAAGAAAGAAA
Db       2139       TGAAGTAAAGTTTGGGGGGAAAAGTTTGGGGGAAAAGTTTCTAGAGAGGTTAAGTTATTTT       2198         Oy       781       ATATATATATATATATATATATATATATATATATATAT	Oy       601       CATGETCETTAAAGGAGAAGATGGGGAGGCATCATTCTCTTACACTTCTGTACACULALA 000         Db       2019       CATGETCETTAAAGGAGAAGATGGGGAAGCATCATTCTGTTACACTTCTGTACACAGTTATA 2078         Oy       661       CATGETCEATCAAAGCCAGACTTGCGTCCATAGTGGAGACTTGCTTTCCAGACAGTAGGA 720         Db       2079       CATGETCEATCAAAGCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCCAGACACTAGGGA 720         Db       2079       CATGETCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTCCAGAACATAGGGA 720         Db       2079       CATGETCTATCAAACCCAGACTTGCTTCCATAGTGGAGACTTGCTTTTCAGAAACATAGGGA 2138         Db       2079       721         TGAAGTAAGGTGCCTGAAAAGTTTCGGGGGAAAAAGTTTCTTTC	AAACTCATCAATAAAACACTACTCCTCTTTCCTCAATCCTCTACCCTTTTCC AAACTCATCAATAAAACACTACTCCTTTTCCTCTACCCCTATTCCTCAATCTTTTACCTTTTC CAAATCCCAATCCCAAATCAGTTTTTTCTCTTTCTTACTCCTCTCCTCCCCTTTTACCCTTTTACCCT 	- 361 1779 421 1839	241 CAAAATTGTGAAGTTAAATTCTCCCACTCTGTCCATCAGATACTATGGTTCTCCCACTATGG 	$\begin{array}{llllllllllllllllllllllllllllllllllll$	$\begin{array}{llllllllllllllllllllllllllllllllllll$	; TYPE: DNA ; ORGANISM: Homo sapiens US-11-120-061-12 Query Match Best Local Similarity 100.0%; Fred. No. 2.1e-48; Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 540	Qy         421         TCTATCACAAGGCCAGTACCACACTCATGAAGAAGAACACAGGAGTAGCTGAGAGGCTA         480           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 1779 TCTCCAACCAAAACATCATCTTTATTAGTTCTGTATACAGGATCTTTGGTCTAC 1838	TCTCCAACCAAAACATCAATGTTTATTAGTTCTGTATACAGTACAGGATCTTTGGTCTAC	Qy         301         CAACTAACTCACTCAATTTCCCTCCTTAGCAGCATTCCATCTTCCCCGATCTTCTTGCT         360           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Characteristic         Charact	1599 ССАСТАВАВАВАТАТАТААТСТСТТАВСАААТТАСАСТСАТТАССАССССАССССТТСА	181 CCA		121 TTTTCTCTTTTACAGGGGAGAATTTCATATTTTACCTGAGCAAATTGATTAGAAAATGGAA	OY       61 TAACTAATCACTTTCCCATCTTTTGTTAGATTTGAATATATACATTCTATGATCATTGCT 120         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         1 AATGAAAGATGGATTTCCAAGGTTAATTCATTGGAATTGAAAATTAACAGGGCCTCTCAC 60	Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Chiefe Match 60 28. 20010 1027. DB 14. Length 245	; DENCIPH: 2458 ; LENGTH: 2458 ; TYPE: DNA ; ORGANISM: Homo sapiens ; ORGANISM: Homo sapiens		FILE REFERENCE: 01997.027700 ; CURRENT APPLICATION NUMBER: US/11/128,049 ; CURRENT FILING DATE: 2005-05-11 ; CURRENT FILING DATE: 2005-05-11 ; PETCE APPLICATION NUMBER: 115 60/570 425		APPLICANT: Leonard, Mark W. APPLICANT: Brown, Eugene L.		APPLICATION NO. US20060010513A1 GENERAL INFORMATION: APPLICANT: Melville, Mark W.	RESULT 14 US-11-128-049-12 ; Sequence 12, Application US/11128049	Db 2439 TAATAAT 2445	QY 1021 TAATAAT 1027	DD 2379 ATCATGTAACTAAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAAATAA 2438	
O) FILDINGLUARD &/ MINUTO V/ CEPT	uery Match est Local Similarity 99.1%; Score 229.8; DB 6; Length 581; arches 731. Concernative O. Mismatches 7. Indels O.	; TYPE: DNA ; ORGANISM: Homo sapiens US-09-925-065A-808251	NO 808251 H: 581	LING DATE: 2001-05-09 DF SEQ ID NOS: 957086 3: FastSEQ for Windows	PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR FILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/289.846	; PRIOR FILING DATE: 2000-11-20 ; PRIOR APPLICATION NUMBER: US 60/250,092 . DETOR DETITION DATE: 2000-11-20	; PRIOR FILLALAN NUMBER: US 00/243,030 ; PRIOR FILLAD DATE: 2000-10-24 ; PRIOR APPLICATION NUMBER: US 60/252,147	; CURRENT APPLICATION NUMBER: US/09/925,065A ; CURRENT FILING DATE: 2001-08-08 ; CURRENT FILING DATE: 2001-08-08	TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135	; GENERAL INFORMATION: ; GENERAL INFORMATION: ; APPLICANT: Wang, David G. ; TITTLE OF THYRATION: Identification and Mapping of Single	RESULT 15 US-09-925-065A-808251 ; Sequence 808251, Application US/09925065A ; buildering 808251, Application US/09925065A	Db 2439 TAATAAT 2445	QY 1021 TAATAAT 1027 .	Oy         961         ATCATTGTAACTAAAAAGCTGACATTGACCCAGACATATTGTACTCTTTCTAAAAATAA         1020           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         901         AGAGCTTGTATGGTTATGGAGGTCTCACCTAGGCATGATTTCACGAAGGCAAGATTGGCAT         960	Qy         841         TATGCGTGTGTGTGTGTAGACACACACGCATACACACATATAATGGAAGCAATAAGCCATTCTA         900	Db 2199 ATATATATATATATATATATATATATATATATATATA	781 ATATATATATATATATATATATATATATATATATATAT	OY       721 TGAAGTAAGGTGCCTGAAAAGTTTGGGGGGAAAAGTTTCTTTC	Oy         661         CATGYCTATCAAACCCAGACTTGCTTCCAAAGACTTGCTTTCAGAACATAGGGA         720	601         CATEGTCGTTAAAGGAGAAGCATCGGGAGCATCATTCTGTTATACTTCTGTACACAGTTATA	Db 1959 CAAATCCCAATCCCCAAATCAGTTTTTCTCTTTCTTACTCCCTCTCTCCCTTTTACCCTC 2018	QY 541 CAAATCCCCAAATCCCCAAATCAGTTTTTTCTCTTTTCTCTCTTTCTCCCCTCTCCCCTTTTACCCCC 600	Db 1899 AAACTCATCAAAAAACACTACTCCTTTTCCTCTACCCTATTCCTCAATCTTTTACCTTTTC 1958	

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1         154         100.0         154         6         AX379349         AX379349         Sequence           3         154         100.0         774         6         AX379345         AX379345         Sequence           4         154         100.0         771         6         AX379345         AX379345         Sequence           5         154         100.0         771         6         AX379345         AX379345         Sequence           6         154         100.0         774         8         AF0325120         AX379345         Sequence           7         154         100.0         1776         6         AX379345         Sequence           6         154         100.0         1776         6         AX379345         Sequence           7         154         100.0         14107         8         AP050154         Acc01481         Homo sapi           7         136.6         80.6         143798         14         Ac146223         Acc146473         Hylobates           11         136.6         85.5         6331         14         Ac146223         Acc146232         Acc146232         Acc146232         Acc146233         Acc146233	the number of than or equa d by analysis d by engle be ry ry ch Length DB	Database : GenEmbl:* 1: gb_ba:* 2: gb_in:* 3: gb_env:* 4: gb_ow:* 5: gb_ov:* 6: gb_pat:* 9: gb_pt:* 10: gb_sts:* 11: gb_y:* 11: gb_w:* 12: gb_un:* 13: gb_ht;* 14: gb_ft;* 15: gb_pl:*	Apr 24 07:43 Copyrig c - nucleic sear April 18, score: 154 : 1 gttgtg table: IDENTITY Gapop 10- : 5883141 s mber of hits sati DB seq length: 0 DB seq length: 20 DB seq length: 20 DB seq length: 20 DB seq length: 20	
ORIGIN         Query Match Best Local Similarity 100.0%; Bred. No. 4.9e-43; Matches 154; CONBERVATIVE 0; Mismatches 0; Indels 0; Gaps 0;         QY       1 GTTTGTGTGCTGCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60 	AUTHORS Miao,C.H. and Kay,M.A. TITLE Liver-specific gene expression cassettes, and methods of use JOURNAL Patent: WO 0199482-A 8 27-DEC-2001; The Board of Trustees of The Leland Stanford Junior University (US) i The University of Washington (US) FEATURES 1154 Source Jorganism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	AX379349 AX379349 AX379349 AX379349 Homo sapie Homo sapie Eukaryota; Hominidae; Hominidae;	<b>B.rge</b> <b>B.rge</b> <b>C</b> 19 104.2 $67.7$ 183536 14 AC 20 21 82 21 82 21 82 21 82 21 82 22 21 82 23 21 82 23 24 25 25 21 82 25 21 82 25 21 82 25 21 82 25 21 82 25 25 21 82 25 25 25 25 25 25 25 25 25 2	Dara

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REFERENCE AUTHORS SOURCE ORGANISM DEFINITION REFERENCE AUTHORS FEATURES BOUTCE DEFINITION SOURCE ORGANISM Query Match Best Local Similarity Matches 154; Conserv TITLE JOURNAL Matches Query Match Best Local source 198 121 138 61 154; 78 Liver-specific gene expression cassettes, Patent: WO 0198482-A 4 27-DEC-2001; The Board of Trustees of The Leland Stanfo ; The University of Washington (US) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; 771 bp Sequence 4 from Patent WO0198482. XX379345 ч Homo sapiens (human) AX379345.1 Liver-specific gene expression cassettes, and methods of Patent: WO 0198482-A 9 27-DEC-2001; The Board of Trustees of The Leland Stanford Junior Unive ; The University of Washington (US) AX379350 328 bp. Sequence 9 from Patent WO0198482. AX379350 Miao, C.H. and Kay, M.A. Miao, C.H. and Kay, M.A. Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens AX379350.1 GI:19575190 Homo sapiens (human) Similarity iominidae; GGAGCTGGGGGCAGAGGTCAGAGACCTCTCTGGGC 154 GTTIGIGIGCIGCCTCIGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA GTTTGTGTGCTGCTCTCAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 60 GGAGCTGGGGCAGAGGTCAGAGACCTCTCGGGC Conservative Conservative /organism="Homo sapiens" /mol\_type="unassigned DNJ /db\_xref="taxon:9606" Location/Qualifiers /organism="Homo sapiens" /mol\_type="unassigned DNJ /db\_xref="taxon:9606" ocation/Qualifiers Homo. GI:19575185 .771 .328 100.0%; 100.0%; Score 154; DB 6; 100.0%; Pred. No. 6.3e-43; tive 0; Mismatches 0; Chordata; Craniata; Vertebrata; Euteleostomi; Buarchontoglires; Primates; Catarrhini; <u>,</u> Score 154; DB 6; Pred. No. 5.5e-43; ; Mismatches 0; DNA" DNA" DNA Stanford Junior University DNA Stanford Junior University 231 and Length Length 328; Indels Indels linear linear methods 771;-0 PAT 18-MAR-2002 PAT 18-MAR-2002 <u>.</u> 0f Сарв Gaps use use 137 (us) 120 197 (us) 0 0 RESULT 5 AX358722 PUBMED REFERENCE ACCESSION VERSION KEYWORDS 뭥 ş 뭥 Ś 뭉 8 RESULT 4 HSU32510 LOCUS ORIGIN Ş ₿ Ş FEATURES REFERENCE SOURCE DEFINITION 昂 昂 Query Match Best Local : Matches TITLE JOURNAL AUTHORS JOURNAL TITLE ORGANISM AUTHORS misc\_signal Bource 201 121 154; 61 198 121 81 61 ч AX358722 n .100.0%; Similarity 100.0%; 54; Conservative 0; Submitted (26-JUL-1995) John Taylor, C Gladstone Institute of Cardiovascular Francisco, CA 9414-9100, USA Location/Qualifiers Hominidae; Homo. 1 (basem 1 to 774) Dang,Q., Walker,D., Taylor,S., Allan,C., Chin,P., Homo sapiens Human apolipoprotein B/C-I Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Homo sapiens (human) U32510.1 HCR-1 HSU32510 Direct Submission Taylor, Dang,Q., Walker,D., Taylor,S., Allan,C., Chin,P., **B/C-I gene locus** Structure of the hepatic control region of the Taylor,J **U32510** 7673250 GGAGCTGGGGCAGAGGGCCAGAGACCTCTCTGGGC 154 GITTIGTGTGCCTCCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA GTTTGTGTGCGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA GGAGCTGGGGGAGAGGGTCAGAGACCTCTCTGGGC 154 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC Biol. Chem. 270 (38), (bases 1 to 774) /standard\_name="HCR-1" /note="APOC1 and APOE genes" /function="hepatic control region" /organism="Homo sapiens" /mol\_type="genomic DNA" . .774 'tissue\_type="placenta" "map="19q" db xref="taxon:9606" chromosome="19" GI:975886 .774 °, Score 154; DB 8; Pred. No. 6.3e-43; ; Mismatches 0; 41907 774 bp -I gene 22577-22585 đ locus, DNA DNA 234 Cardiovascular r Disease, P.O. (1995) 231 hepatic control region Length 774; Indels linear linear human apolipoprotein Fan, J. Fan, J. and PAT 13-FEB-2002 Disease, Box 419100, PRI 31-JAN-1996 0 and Gaps 120 140 200 60 San 0

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Direct Submit Submitted (22 Instrumentati Subiaco, WA 6 3 (bases 1 t Dawking,R.L. Direct Submits Submitted (25 Instrumentati Nedlands, WA On Jan 5, 199 On Jan 5, 199 Ce /org	<pre>Mammalia; Butheria; Buarchontoglires; Primates; Cata Hominidae; Homo. 1 (bases 1 to 41907) Preitas, E.M., Zhang, W.J., Lalonde, J.P., Tay, G.K., Ga Ashworth, L.K., Van Bockxmeer, F.M. and Dawkins, R.L. Sequencing of 42kb of the APO B-C2 gene cluster revy PEREC1 DNA Seq. 9 (2), 89-100 (1998) 10520737 2 (bases 1 to 41907) 2 (bases 1 to 41907) Preitas, E.M. and Zhang, W.J.</pre>	41907 bp DNA P19374 APO B-C2 gene 701 )	61 36968 121 37028	ORIGIN Query Match 100.0%; Score 154; DB 6; Length 41907; Best Local Similarity 100.0%; Pred. No. 1.1e-42; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GTTNGTGTGCTGCTGCAGTCCACACTGAACAAACTTCAGGCTACTCATGTCCCTAAA 60 	REFERENCE 1 AUTHORS Stanton,V.P. TITLB Methods for genetic analysis of dna to detect sequence variances JOURNAL Patent: WO 0190419-A 100 29-NOV-2001; Variagenics, Inc. (US) ; Stanton; Vincent P., Jr. (US) FEATURES Location/Qualifiers Source /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"	M 33 0
<pre>SHALGARK ULARY OULS DY VOULS DY VO</pre>	<pre>mRNA</pre>	AGPPPPPAALVGLPP EDGACGCLPNPGTFEE NYHPGVTYVGTKQLSP NYHPGVTYVGTKQLSP GYTQLDLPKANLLPKGS IG" IG"	CDS join(4287.4560,5264.5331,5708.5800,6651.6752, 6832.6937,13297.13419,13595.13671,13775.13877, /gene="D195117E" /note="C1889.6 homolog; Alias: PEREC1" /product="D195117E" /product="AAD02504.1"	/translation="QEMPRYHELPTLEERSGELHPGATSLGSPIPVPGGPPAVEDVSL DLEDERGESEKTLDKINPIYDALSYSSPSDSYQGKGFVMSRAMYV" 4000.16000 /gene="D19S1177E" mRNA 501(44287.4560,52645331,57085800,66516752, 5597515736] /gene="D19S1177E"	<pre>gene /gene="pRR2" mRNA &lt;978&gt;1250 CDS /gene="pRR2" /note="PRR2" /codon_start=1 /product="poliovirus receptor family" /product="poliovirus receptor related protein 2" /product="c1:4105702"</pre>	/mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="19" /map="l9q13.2" /clone="cosmid F19374" /note="Sequence was obtained from the shotgun sequencing of the cosmid clone, F19374. This clone was kindly provided by the Lawrence Livermore National Laboratories, CA"

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RESULT 7 AC011481 REFERENCE AUTHORS SOURCE . REFERENCE 8 Ş 뎡 Ş 昂 Ś COMMENT REFERENCE DEFINITION ORIGIN GRYWORDS /ERSION ACCESSION SCC S AUTHORS TITLE JOURNAL TITLE TITLE JOURNAL Matches 154; AUTHORS Query Match JOURNAL Best gene gene Sg3 g Local 37028 36968 36908 121 61 Direct Submission Submitted (29-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 29, 2001 this sequence version replaced gi:8576069. Draft Sequence Produced by DOE Joint Genome Institute Direct Submission Submitted (07-OCT-1999) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 3 (bases 1 to 107567) DOB Joint Genome Institute and Stanford Human Genome Center. Homo sapiens chromosome AC011481 AC011481.4 GI:13487947 ч HIG Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.4. Ното варіепя STS Content: SHGC-11493 G14568 www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center 1 (bases 1 to 107567) DOE Joint Genome Institute and Stanford Human Genome Center. Hominidae; Homo. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homo sapiens (human) AC011481 ww-shgc.stanford.edu 2 (bases 1 to 107567) DOB Joint Genome Institute. Unpublished Similarity irect Submission GTTTGTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154 GGAGCTGGGGGAGAGGTCAGAGACCTCTCTGGGC 37061 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 36967 Conservative /translation="MRLPLSLPVLVVVLSIVLBGPAPAQGTPDVSSALDKLKBFGNTL BCKARELIERIKQSELSAKMREWFSETFQKVKEKLKIDS" codon\_start=1 pseudo 'gene="APOC1'" pseudo gene="APOC1'" codon\_start=1 gene="HCR-1" 6828. pseudo 'gene="HCR-1" 6828. .37547 db\_xref="GI:4105705" note="apolipoprotein pseudo note="Hepatic control region 1" 100.0%; 100.0%; .37547 <u>,</u> Score 154; DB 8; Pred. No. 1.1e-42; Mismatches 0; C1 pseudogene" DNA Length 41907; linear Indels complete sequence. PRI 29-MAR-2001 <u>,</u> DOE Joint 94598, USA Gaps 0 REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE RESULT 8 AC021988 Ş COMMENT REFERENCE 昂 Ś 昂 B Ş ACCESSION DEFINITION LOCUS ORIGIN FEATURES ORGANISM Matches 154; JOURNAL TITLE AUTHORS Query Match Best JOURNAL BOUTCE Local Similarity 67289 67229 67169 Center project name: H\_NH004C16 Sequencing vector: M13; 95% Sequencing vector: plasmid; 5% Chemistry: Dye-primer ET; 95% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 192142 bases at least Q40 Consensus quality: 192142 bases at least Q40 Consensus quality: 200851 bases at least Q20 Insert size: 198000; agarose-fp Quality coverage: 5.02 in Q20 bases; agarose-fp Quality coverage: 4.88 in Q20 bases; sum-of-contigs 121 ព្ Direct Submission Submitted (23-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. 208239 bp Homo sapiens chromosome 19 clone SEQUENCE, 16 unordered pieces. AC021988 ч Center: Washington University Genome Sequencing Center Center code: WUGSC MO 63108, USA On Jun 16, 2000 this sequence version replaced gi:7230864 web site:http://genome.wustl.edu/gsc/index.shtml
------ Project Information -------2 (bases 1 to 208239) Waterston, R.H. 1 (bases 1 to 208239) Waterston,R.H. The sequence of Homo sapiens clone Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Buthria; Buarchontoglires; Primates; Catarrhini; Homo sapiens AC021988.4 GI:8569766 HTG; HTGS\_PHASE1; HTGS\_DRAFT. Homo sapiens (human) Unpublished SHGC-89260 G53983 iominidae; Homo. NOTE: GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 67322 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154 Conservative This /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" /chromosome="19" 'clone="CTB-129P6" ocation/Qualifiers .107567 18 100.0%; S 100.0%; P 1100.0%; P ø 'working Genome Center -----Score 154; Pred. No. 1 Mismatches draft' sequence. It currently DNA li RP11-84C16, 1.3e-42; DB 8; <u>,</u> Length 107567; linear Indels WORKING HTG 07-JUL-2000 G DRAFT 0 .: Gaps Louis, 120 67288 67228 60 0

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PEATURES gap gap gap gap gap misc\_feature gap misc\_feature Bource misc\_feature misc\_feature misc\_feature misc\_feature misc\_feature consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence. ğ as soon as it is available and the accession number will 88898 107699 134678 88798 163260 134578 107799 58086 72522 preserved. 7262: 57986 46559 46459 13439 38140 13539 1608 1708 29748 9648 2132 5456 8040 /note="assembly\_name:Contig20
clone\_end:T7 /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" /chromosome="19" 1. .208239 /note="assembly\_name:Contigl8"
13439. .13538 7748. .13438 3449 rector\_side:right" 22232. 22132. .22231 estimated\_length=unknown estimated OCATION/ 'estimated\_length=unknown 13539 note="assembly\_name:Contig17" '648. .7747 estimated 608 note="assembly\_name:Contig13" estimated\_length=unknown 556. note="assembly\_name:Contig16" note="assembly\_name:Contig15" note="assembly\_name:Contig19" estimated clone="RP11-84C16" 58085: gap of unknown length 72221: contig of 1436 bp in length 72621: gap of unknown length 88797: contig of 16176 bp in length 107698: contig of 18001 bp in length 107798: gap of unknown length 134577: contig of 26779 bp in length 134577: gap of unknown length 163159: contig of 28482 bp in length 163259: gap of unknown length .1607 .ımated\_length=unknown ). .5455 208239: contig of 44980 13438 3803 1353 mated\_length=unknown .7647 46558 7647 5555: 5455: 3448: 3348: 1707: 1607: .3348 .29647 .2213 1707 'Qualifiers \_length=unknown gap gap gap of contig contig of 2092 gap of unknown contig of 1641 gap of unknown contig of 1607 gap of unknown gap of unknown contig of 8319 bp in gap of unknown length contig of 11427 bp gap of unknown contig of 8292 contig of 7416 contig unknov unknor of 8593 unknown of 5691 bp in length bp in length bp in length bp in length bp in bp in length ut đạ ni dq length length đđ length length length length rengrn ength H in length length length length length length SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 9 AC146473 Ś 망 Ş ₽ 昂 Ş ORIGIN DEFINITION REFERENCE Snoo Query Match Best Local Similarity Matches 153; Conserv JOURNAL TITLE AUTHORS gap gap gap gap gap gap gap gap gap misc\_feature misc\_feature misc\_feature misc\_ misc\_feature misc\_feature misc\_feature misc\_feature misc 26223 26164 26104 feature 121 feature 61 ч Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Peng,Z., Malinov,I. and Rubin,E.M. Direct Submission Unpublished AC146473 39483 bp DNA Hylobates klossii clone RZ140-83M19, W ordered pieces. AC146473.1 GI:33695020 HTG; HTGS\_PHASE2; HTGS\_DRAFT. HYlobates klossii (Klossis gibbon) Hylobates klossii Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hylobatidae; Hylobates. AC146473 GITTOTOTOTOCTOCTOTAAGTCCACACIGAACAAACTTCAGCCTACTCATGTCCCTAAA GGAGCTGGGGGCAGAGGTCAGAGACCTCTCTGGGC GTTTGTGTGCCTCCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60 GEAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC (bases 1 to 39483) Conservative /estimated\_length=unknown 163260. .208239 /note="assembly\_name:Contig29" 29748. .38039 29648. 38898. .107698 /estimated length=unknown
34678..163159 /estimated length=unknown
07799. .134577 note="assembly\_name:Contig26" 07699. .107798 estimated length=unknown 6559...57985 8140. .46458 note="assembly\_name:Contig21" note="assembly\_name:Contig28" 63160. .163259 estimated\_length=unknown estimated length=unknown 8086. .72521 6459. .46558 estimated\_length=unknown 34578. note="assemb. estimated\_length=unknown :e="assembly\_name:Contig24" e="assembly\_name:Contig23" e="assembly\_name:Contig22" 92.2**%;** 99.4**%;** e="assembly\_name:Contig25" 3. .88897 imated\_length=unknown .88797 .72621 .38139 .29747 .58085 assembly\_name:Contig27" .134677 <u>,</u> Score 142; DB 14; Pred. No. 2.5e-38; D; Mismatches 0; 26256 154 NA linear HTG 16-AUG-2003 WORKING DRAFT SEQUENCE, 2 °; Length 208239; Indels Hosseini, R., 1; Gaps

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RESULT 10 AC145523 LOCUS AC145523 183798 bp DNA linear HTG 05-AUG-2003 DEFINITION Papio hamadryas clone RF41-112M21, WORKING DRAFT SEQUENCE, 4	31974		Qy       1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 60         Db       31854 GTTTGTGTGCTGCCTCTGAAGTCCACCCTGAACAAACCTTCAGCCTGCTCCTGTCCCTAAA 31913	Query Match 91.7%; Score 141.2; DB 14; Length 39483; Best Local Similarity 94.8%; Pred. No. 3.8e-38; Matches 146; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	/db_xref="taxon:9587" /clone="RZ140-83M19" 2211022209 ORIGIN /estimated_length=unknown	rce	<ul> <li>1 22109: contig of 22109 bp in length</li> <li>22110 22209: gap of unknown length</li> <li>22210 39483: contig of 17274 bp in length.</li> </ul>	<ul> <li>of the gaps between them are based on estimates that have</li> <li>provided by the submittor:</li> <li>This sequence will be replaced</li> <li>by the finished sequence as it is available and</li> <li>the accession much will be propagate to available and</li> </ul>	Chemistry: Dye-ceritation Big Dye Assembly program: Phrap version 0.990329. * NOTE: This is a 'working draft' sequence. It currently * consists of 2 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces * is believed to be correct as given, however the sizes	Funding agent: Programs for Genomic Applications (NHLBI) Summary Statistics:	The order-orientation of the draft sequence was accomplished by using: Avid (http://baboon.math.berkeley.edu/mavid), Lagan (http://lagan.stanford.edu/) and paired end information.	This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be viewed at: http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2	Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov Center Code: PGABERK Center Project Name: IO05 Bac Clone Name: R2140-83M19	REFERENCE 2 (bases 1 to 39483) AUTHORS Cheng,JF., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R., Peng,Z., Malinov,I. and Rubin,E.M. TITLE Direct Submission JOURNAL Submitted (16-AUG-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
gap	FEATURES	• • • •	* * * *	• • * * 5	- Su AB			Th via	, Web Cen Bac	AL			REFERENCE 1 AUTHORS C TITLE D:	ACCESSION AN VERSION AN KEYWORDS P SOURCE P ORGANISM P
/organism="Papio hamadryas" /mol_type="genomic DNA" /db_xref="taxon.9557" /clone="RP41.112M21" 5994560044 /estimated_length=unknown	108287 108387; 198387; 198387 of 10K10W1 Length 168387 171995; contig of 3609 bp in length 171996 172095; gap of unknown length 172096 183798; contig of 11703 bp in length. Location/Qualifiers 1183798	59944: contig of 59944 60044: gap of unknown 168286: contig of 10824	replaced uence as soon as it is r will be preserved.	consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have	Summary Statistics: Sequencing vector: Plasmid; pUC18 Chemistry: Dye-terminator Big Dye Assembly program: Phrap version 0.990329. * NOTE: This is a 'working draft' sequence. It currently	ions (	rder-orientation of the draft sequence was accomplishes (http://baboon.math.berkeley.edu/mavid), (http://baboon.math.berkeley.edu/mavid),	This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be viewed at: http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2	Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov Center Code: PGABSRK Center Project Name: 8056 Bac Clone Name: RP41-112M21	Submitted (05-AUG-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA On Aug 5, 2003 this sequence version replaced gi:32996764.	Rd., Berkeley, CA 94720, L ., Peng,Y., Mukherjee,S., F Rubin,B.M.	<pre>Conjustion (bases 1 to 183798) 2 (bases 1 to 183798) Cheng,JF., Hamilton,M., Peng,Y., Mukherjee,S., Hosseini,R., Peng,Z., Malinov,I. and Rubin,B.M. Direct Submission Direct Submission Submitted (19-JUL-2003) Genome Sciences, Lawrence Berkeley National Submitted (19-JUL-2003) Genome Sciences, Lawrence Berkeley National</pre>	<pre>pressure a successive successing successis successive successive successive success</pre>	AC145523 AC145523.2 GI:33438604 HTG; HTGS PHASE2; HTGS DRAFT. PHJG hamadryas (hamadryas baboon) Papio hamadryas (hamadryas baboon) Papio hamadryas (hordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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The order-orientation of the draft sequence using: Avid (http://baboon.math.berkeley.edu/mavid) Lagan (http://lagan.stanford.edu/) and paire Punding agent: Programs for Genomic Applicat Summary Statistics: Sequencing vector: Plasmid; pUC18 Chemistry: Dye-terminator Big Dye Assembly program: Phrap version 0.990329. • NOTE: This is a 'working draft' sequence. • consists of 8 contigs. Gaps between the co * are represented as runs of N. The order of	Match ocal Si ocal Si ocal Si (62213 c (62273 A (62273 A (62273 A (62273 A (145; (1	gap 168287168386 /estimated length=unknown gap 171996172095
ion of the draft sequence was accomplished by on.math.berkeley.edu/mavid), in.math.cerkeley.edu/mavid), in.math.cerkeley.edu/mavid), sprams for Genomic Applications (NHLBI) is in plasmid; pUC18 minator Big Dye Phrap version 0.990329. "working draft' sequence. It currently "working draft' sequence. It currently "working draft' sequence. It currently "working draft' sequence of the pieces	<pre>/estimated_length=unknown /estimated_length=unknown similarity 94.2%; Pred. No. 1.8e-37; Indels 0; Gaps 0; Id= Conservative 0; Mismatches 9; Indels 0; Gaps 0; Id= Conservative 0; Id= Conservative Conservation Id= Conservative 0; Id= Conservative Conservation Id= Conservative 0; Id= Conservative Conservative Conservative Conservative Conservative 0; Id= Conservative Conserver Conservative Conservative</pre>	
RESULT 12 HSU35114 LOCUS DEFINITION ACCESSION VERSION VERSION ORGANISM Homo sapiens ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homo. REFERENCE 1 (bases 1 to 4097)	<pre>Partness P</pre>	• • • •

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REFERENCE AUTHORS REFERENCE AUTHORS RESULT 13 AC120211/c ORIGIN PUBMED REFERENCE AUTHORS TITLE COMMENT 昂 Ś 昂 Ş 昂 ą ORGANISM KEYWORDS FEATURES SOUICE VERSION ACCESSION DEFINITION Scos JOURNAL TITLE TITLE Query Match Best Local Similarity Matches 140; Conserv AUTHORS TITLE JOURNAL **JOURNAL** JOURNAL gene misc\_signal 121 252 132 GITTIGIGIGCIGCCICIGAAGICCACCCIGAAIGACCITCAGCCIGITCCCCGICCCIGAT 191 Submitted (04-MAY-2002) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA Draft Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov Center Code: PGABERK Pan 1 (bases 1 to 63931) Martin,J., Hosseini,R., AC120211.1 GI:20451083 HTG; HTGS PHASE1; HTGS DRAFT. Pan troglodytes (chimpānzee) Pan troglodytes 1 GTTTGTGTGCCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60 Dang,Q. and Taylor,J. In vivo footprinting analysis of the hepatic control region of the human apollopoprotein B/C-I/C-IV/C-II gene locus J. Biol. Chem. 271 (45), 28667-28676 (1996) Direct Submission Eukaryota; Metazoa; Chordata; Craniat; Mammalia; Eutheria; Euarchontoglires; Submitted (30-AUG-1995) John Taylor, Cardiovascular, Gladstone Institute, P.O. Box 419100, San Francisco, CA 94141-9100, USA Comparative analysis and ordering by homology are available here: http://pga.lbl.gov/cgi-bin/search\_cvcgd?type=n&value=APOE Cheng, J.-F. 2 (bases 1 to 63931) Martin,J., Hosseini,R., Unpublished Direct Cheng, J. - P. Hominidae; Pan. AC12021 unordered pieces. AC120211 Direct Submission Additional information: Allan, C.M., Walker, D. and Taylor, J.M GGAGCTGGGGCAGAGGGTCAGAGACCTCTCTGGGC 154 GGAGCTGCGGCAGAGGTCAGAGACCTCTCAGGGC (bases 1 to 4097) 63931 bp troglodytes clone RP43-174J24, . 85.5%; llarity 90.9%; Conservative Submission /note="DNA sequenced was from a Pl plasmid clone from human genomic library from Genome Systems, Inc., St. Louis, MO; chromosome 19q" Location/Qualifiers gene="APOE" 'standard\_name="HCR-2" 'function="hepatic control region" 'gene="APOS" /organism="Homo sapiens"
/mol\_type="genomic DNA"
/db\_xref="taxon:9606" .4097 .4097 <u>,</u> Score 131.6; DB 8; Pred. No. 6.7e-35; D; Mismatches 14; Peng,Y., Peng,Y., Craniata; Vertebrata; Euteleostomi; oglires; Primates; Catarrhini; Peng, Z., Peng, Z., DNA WORKING 285 Rubin,E.M. Rubin, E.M. and linear HTG 04-MAY-2002 DRAFT SEQUENCE, 20 Length 4097; Indels and 0; Gaps 120 251 ω <u>,</u> FEATURES gap gap gap gap gap gap gap source Assembly program: Phrap version 0.990329. NOTE: This is a 'working draft' sequence. It currently \* consists of 20 contigs. The true order of the pieces \* is not known and their order in this sequence record is \* arbitrary. Gaps between the contigs are represented as \* runs of N, but the exact sizes of the gaps are unknown. \* This record will be updated with the finished sequence. Funding agent: Programs for Genomic Applications Contact: 'Jody Schwartz' jrschwartz@lbl.gov Summary Statistics Sequencing vector: Plasmid; pUC18 Chemistry: Dye-terminator Big Dye as soon as it is available and the accession number will be preserved. 42366 45544 49571 49571 53134 53234 60428 38305 38405 42266 31938 32038 14253 17634 17734 34828 27305 25123 27205 21152 34728 29787 29687 14153 006TT 25023 21052 12000 2247 2347 E169 4721 4621 2247 /estimated\_length=unknown 17634. .17733 /estimated\_length=unknown 14153. .14252 /organism="Pan troglodytes" /mol\_type="genomic DNA" /db\_xref="taxon:9598" location estimated estimated estimated\_length=unknown estimated length=unknown 621. 'clone="RP43-174J24" 1900. estimated\_length=unknown .6393 .4720 63931: 60527: 60427: 53233: 2978¢ 25122 11999 .9235 .2346 1967 10643: 12365: 12265: 3472 2720 2502 2105 1773 1425 1415 1189 1763 9235 551 6912: 4720: 4620: 2346: 2246: .119999 /Qualifiers \_length=unknown length=unknown gap of contig contig gap of contig contig of 2246 gap of unknown contig of 2274 gap of gap of gap of contig gap of gap conti gap gap conti gap gap gap contig contig contig contig gap of contig contig gap of gap of contig gap of gap of contig cont contig gap of contig of 2192 o g ĉ 0 0 E <u>0</u> of unknown ig of 3463 j of 3178 of 2382 g of 2153 ĉ of 7194 of 3861 0f of 2690 unknown of 3927 Р, ę, of 2123 unknown unknown unknown unknown unknov unknown of 2151 unknown of 2082 unknown unkno of 3318 unknown unknown of 2664 unknown unknown of 2246 3404 3477 3871 3381 bp in bp in Å ģ lengtn g đ bp in bp in length ni dq ni dq ģ Length hp in ĥ bp in nt dq uī dq 9 b length bp in ģ length bp in Length length bp in length length length length Lengtn length Length length length length rengtn Length In H in 11 in length H ĥ length (NHLBI)

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JOURNAL Submitted (05-AUG-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA	Cneng,JF., Hamilton,M., Feng,Y., Wanneijee,J., Woodens, Peng,Z., Malinov,I. and Rubin,B.M. Direct Submission	Laboratory, 1 Cyclotron kd., Berkerey, c4 94/20, 3 (bases 1 to 183798) 3 (bases 1 to 183798)	003) Genome Sciences, L		Direct Submission Unpublished	AUTHORS Cheng, JF., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R., Peng, Z., Malinov, I. and Rubin, E.M.		Papio hamadryas (hamadryas papoon) 3M Papio hamadryas	AC1455	ő					3271	. 61	QY       1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 60	; Conservative 0; Mismatches 14; Indels 0; Gaps	DB 14; Length 63931; 34;	ORIGIN	gap ovrzeovzz/ /estimated_length=unknown				ran /estimated_length=unknown 4554445643			gap 34728. 34827			/ eBC1maced_religen=unknown gap 27205. 27304	/ 6851maced_1engch=uukuvwu gap 2502325122	gap 2105221151
RESULT 15 AC146285		66		ОУ рь 670	Db 670	8	Query Match Best Local 1 Matches 13	ORIGIN	gap	gap	gap		source	FEATURES										•									COMMENT
· · · ·		942 GGAACTGGGGCAGAGGTCAGAGAGCTCCCTGGGC 66909	121	61         ATGGGCAAACATTGCAAGCAGGCAAACAGCACAGGCCCTGCCTG	062	AGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA	tch 84.4%; Score 130; DB 14; Length 183798; al Similarity 90.3%; Pred. No. 4.4e-34; 139; Conservative 0; Mismatches 15; Indels 0; Gaps 0;		/r1996172095 /estimated length=unknown	168287158386 /estimated length=unknown	/ctude AF4 5994560044 /estimated length=unknown	/ol_type="genomic DNA" /db_xref="taxon:9557" /-I_Type=taxon:9557"		<ul> <li>171996 1172095: gap of unknown zenyth</li> <li>172096 183798: contig of 11703 bp in length.</li> <li>Location/Qualifiers</li> </ul>	<ul> <li>60045 100200 Course of account of a course of a cours</li></ul>	59945	<ul> <li>this sequence as soon as it is available and</li> <li>by the finished sequence as soon as it is available and</li> <li>the accession number will be preserved.</li> <li>the source of the sou</li></ul>		<ul> <li>are represented as runs OI N. The order of the sizes</li> <li>is believed to be correct as given, however the sizes</li> <li>cf the case between them are based on estimates that have</li> </ul>	* consists of 4 contigs. Gaps between the contigs	Assembly program: Phrap version 0.990329. * NOTR: This is a 'working draft' sequence. It currently	Sequencing vector: Plasmid; pucts Chemistry: Dye-terminator Big Dye	Summary Statistics:	Funding agent: Programs for Genomic Applications (NHLBI)	Avid (http://baboon.math.beinery.euv/marrey, Lagan (http://lagan.stanford.edu/) and paired end information.	using: 	The order-orientation of the draft sequence was accomplished by	viewed at: http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=APOC2	This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be	Bac Clone Name: RP41-112M21	Center Code: PGABERK Center Project Name: B056	Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov	

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REFERENCE AUTHORS VERSION KEYWORDS SOURCE REFERENCE AUTHORS COMMENT REFERENCE DEFINITION Locus CCESSION TITLE JOURNAL TITLB TITLE ORGANISM JOURNAL JOURNAL AUTHORS If the Bac Library Name is LB1 to LB4, please see website for the description: http://www-gsd.lbl.gov/cheng/BAC.html These libraries are available through the BACPAC Resources Center: http://www.chori.org/bacpac/libraryres.htm as LBNL-1 to LBNL-4. Assembly program: Phrap version 0.990329. NOTE: This is a 'working draft' sequence. It currently • consists of 6 contigs. Gaps between the contigs • are represented as runs of N. The order of the pieces • is believed to be correct as given, however the sizes • of the gaps between them are based on estimates that have • provided by the submittor. • This sequence will be replaced Summary Statistics: using: Avid (http://baboon.math.berkeley.edu/mavid), Lagan (http://lagan.stanford.edu/) and paired end information. This sequence has been compared to sequences of other species using Vista (http://www-gsd.lbl.gov/VISTA). The results can be viewed at: Sequence Produced by Berkeley PGA web site: http://pga.lbl.gov Center Code: PGABERK Center Project Name: T019 Sequencing vector: Plasmid; pUC18 Chemistry: Dye-terminator Big Dye Funding agent: Programs for Genomic Applications (NHLBI) The order-orientation of the draft sequence was accomplished by Submitted (07-AUG-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA Cheng, J.-F., Hamilton, M., Peng, Y., Peng, Z., Malinov, I. and Rubin, B.M. Submitted (02-AUG-2003) Genome Sciences, Lawrence Berkeley National Laboratory, 1. Cyclotron Rd., Berkeley, CA 94720, USA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae; Callicebinae; Callicebus 1 (bases 1 to 185724) AC146285 185724 bp 1 Callicebus moloch clone LB5-404K13, http://pga.lbl.gov/cgi-bin/search\_cvcgd?type=n&value=APOC2 Bac Clone Name: LB5-404K13 Laboratory, 1 Cyclotron Ru., Bernary, \_\_\_\_\_ On Aug 7, 2003 this sequence version replaced gi:33413350 Direct Submission Direct Submission Cheng, J.-F., Hamilton, M., Peng, Z., Malinov, I. and Ru Peng,Z., Malinov, Direct Submission Cheng,J.-F., Hamilton,M., Peng,Y., Mukherjee,S., Peng,Z., Malinov,I. and Rubin,E.M. Callicebus moloch (Dusky titi) Callicebus moloch HTG; HTGS\_PHASE2; HTGS\_DRAFT AC146285 ordered pieces. AC146285.2 GI:33469171 aboratory, 1 Cyclotron (bases 1 to 185724) by the finished sequence as soon as it is available the accession number will be preserved. 1 6536 bp in length 6537 6636: gap of unknown length 54160 54259: contig of 47523 bp in length 54260 76479: contig of 2220 bp in length 76480 76579: gap of unknown length 76580 110159: contig of 33580 bp in length 'npublished (bases 1 to 185724) ., Peng,Y., Rubin,B.M. Mukherjee,S., Hosseini,R., Mukherjee,S., DNA linear HTG 07-, WORKING DRAFT SEQUENCE, Hosseini,R., Hosseini, R., HTG 07-AUG-2003 and ო Чo Ъ Ե Search completed: April 18, 2006, 14:56:52 昂 Ş 8 昂 Ş ORIGIN FEATURES Matches 138; Query Match Best Local Similarity time : 848.062 secs gap gap gap gap gap Bource 148162 148102 148042 117 61 μ GITTIGOGIGCIGCCICIGAAGICCACCCIGAACGACCTICAGCCIGTICCCIGICCCIGAG 148101 CCTGGGAGCTGGGGGCAGAGGTCAGAGACCTCCCGGGCC 148199 CCTTGGAGCTGGGGGCAGAGGTCAGAGACCTCTCTGGGGC 154 ATGGGCAAACATTGCAAG----CAGCAAACAGCAAAACACACCCCTCCCTGCCTGCTGA 116 GITTGIGIGCTGCCTCTGAAGTCCACACIGAACAAACTTCAGCCTACTCATGTCCCCTAAA 60 133024 133124 110160 110260 Conservative 6537 /organism="Callicebus moloch" /mol\_type="genomic DNA" /db\_xref="taxon:9523" /cl\_one="LB5-404K13" /estimated\_length=unknown 133024. .133123 'estimated\_length=unknown estimated le 6480. .76579 ocation/Qualifiers estimated\_length=unknown 4160. estimated\_length=unknown 10160. .185724 110259: gap of unknown length 133023: contig of 22764 bp in length 133123: gap of unknown length 185724: contig of 52601 bp in length. 74.3%; .6636 .54259 .110259 <u>,</u> length=unknown Score 114.4; DB 1. Pred. No. 1.4e-28; 0; Mismatches 16 DB 14; Length 185724; 16; Indels

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	Pred. score and i Result No. Sc	Database	OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Searched: Total number of Minimum DB seq 1 Maximum DB seq 1 Post-processing:
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1100.0 100.0 10	No. is the r greater thar derived by Query Query Dre Match L	N N N N N N N N N N N N N N N N N N N	Copyright nucleic search, April 18, 20 US-09-884-90 : 154 1 gtttgtgtgc : 154 Gapop 10.0 , 4996997 seqs of hits satisfy of hits satisfy iq length: 20000 iq length: 20000 iq length: 20000
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<pre>(GTRD ) UNIV LELAND STANFORD JUNIO (UNIW ) UNIV WASHINGTON. Miao CH, Kay MA; wpi; 2002-114582/15. Mucleic acid construct for express mammalian liver cells, has operabl hepatic promoter, coding sequence, Example 2; Page 59; 64pp; English. The present sequence is that of an apolipoprotein B gene. The enhance cassettes of the invention designe Factor IX. The cassettes also incl located 5: to a liver-specific pro- located sy to a signal, and an</pre>	98482-A2. -2001. -2001, 2001V -2000, 2000	andarc (fi) poprot poprot plood	22222222222222222222222222222222222222
LELAND STANFORD JUNIOR. WASHINGTON. Y MA; construct for expressin ver cells, has operably oter, coding sequence, p oter, coding sequence, p sequence is that of an e in B gene. The enhancer the invention designed be casestes also include con signal, and an ir	A2. 2001WO-US019634. 2000US-0212902P.	DNA; 15 it entry) sin E gen ApoB; er ilotting;	- 88 81 12 20 70 70 70 70 70 70 70 70 70 70 70 70 70
ORD JU or expr sequen sequen Engli hat of also i also i also i also i	1634.	154 BP. (TY) Jene enh Jg; gene	2 AAV 2 AAV 2 AAV 2 AAV 2 AAV 2 AAV 2 AAV 2 AAV 2 AAV 2 AAV 4 AAV
<pre>) UNIV LELAND STANFORD JUNIOR. ) UNIV WASHINGTON. H, Kay MA; 002-114582/15. c acid construct for expressing nucleic acid molecules, proteins in ian liver cells, has operably linked hepatic locus control element, c promoter, coding sequence, polyadenylation signal and intron. c promoter, coding sequence, polyadenylation signal and intron. e 2; Page 59; 64pp; English. e 2; Page 59; 64pp; English. esent sequence is that of an enhancer sequence from the human oprotein B gene. The enhancer may be incorporated into expression tes of the invention designed for liver-specific expression of tes of the invention designed for liver-specific control region iX. The cassettes also include an hepatic locus control region d 5' to a liver-specific expression of d si to a signal, and an intron (see AAI71003-16). Also provided</pre>		py;	AAV19600 ADU47590 ADU47590 ADU47590 ADU47580 AAV15389 AAV1598 AAV1598 AAV1598 AAV1598 AAV1598 AAV1598 AAV1959
d molecules, proteins in c locus control element, n signal and intron. nce from the human orated into expression offic expression of locus control region IX coding sequence, a 71003-16). Also provided		expression cassette; liver;	Aav19600 Apolipopr Aav15305 ApoB enha Adu47590 Oligonucl Aav15398 Apolipopr Aav15389 ApoB enha Aav15389 ApoB enha Aav15387 ApoB enha Adu47588 Oligonucl Aav15383 ApoB enha Adu47584 Oligonucl Aav15383 ApoB enha Adu47586 Nigonucl Adu73621 Human cDN Abz14763 Genomic D Abz75079 Human foe Aat55613 Probe #18 Aak49722 Human bra Abs49348 Human liv Abs423514 Human foe Aat4244 Probe #18 Aak36772 Human bra Aak10914 Human bra

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<pre>Miao CH, Kay MA; XX WPI; 2002-114582/15. Nucleic acid construct for expressing nucleic acid PT mammalian liver cells, has operably linked hepatic PT hepatic promoter, coding sequence, polyadenylation PS Bxample 2; Page 59; 64pp; English. XX Example 2; Page 59; 64pp; English. XX CC The present sequence is that of the hepatic locus CC The present sequence is that of the hepatic locus CC capression cassettes of the invention designed for expression of Factor IX. The cassettes also includ located 3' to the hepatic locus control element, the sequence, a 3' polyadenylation signal, and an intr CC hepatic promoter and 5' to the polyadenylation signal.</pre>	SULT 2 IJI010 AAIJ1010 standard; DNA; 328 AAIJ1010; 18-MAR-2002 (first entry) Human apolipoprotein E gene Apolipoprotein E; ApoE; hepa expression cassette; liver; Homo sapiens. WO200198482-A2. 27-DEC-2001. 19-JUN-2001; 2001WO-US019634 20-JUN-2000; 2000US-0212902P (STRD ) UNIV LELAND STANFORD (UNIW ) UNIV WASHINGTON.	CC       are vectors that include an expression cassette         CC       may episomal or integrating vectors, including         CC       used in a claimed method of ameliorating Pactor IX         CC       used in a claimed method of ameliorating Pactor IX         CC       therapeutic amount of blood clotting Pactor IX was         CC       examples of the invention, human Pactor IX was         CC       expression cassettes into the tail vein or port         CC       expression cassettes into the tail vein or port         CC       expression cassettes into the tail vein or port         SQ       Sequence 154 BP; 40 A; 47 C; 36 G; 31 T; 0 U; 0         Query Match       100.0%; Score 154; DB 6;         Best Local Similarity       100.0%; Pred. No. 7.16-0         Matches       154; Conservative       0; Mismatches         QV       1       GTTTGTGTGTCGCCTCTGAAGTCCAACACTGAACAAAACT         QV       1       GTTTGTGTGCGCCTCTGAAGCAACAAACACAAAACT         QV       1       GTTTGTGTGGCCAAACATTGCAAGCAAGCAAACACAAAACAAAACT         QV       61       ATGGGCAAACATTGCAAGCAAGCAACACAAAACAAAAACAAAAAAACAAAAAA
Miao CH, Kay MA; WPI; 2002-114582/15. WPI; 2002-114582/15. Wucleic acid construct for expressing nucleic acid molecules, proteins in nammalian liver cells, has operably linked hepatic locus control element, hepatic promoter, coding sequence, polyadenylation signal and intron. Example 2; Page 59; 64pp; English. The present sequence is that of the hepatic locus control element of the numan apollpoprotein B gene. The sequence can be incorporated into expression casestees of the invention designed for liver-specific promoter IX. The casestees also include an hepatic promoter located 3' to the hepatic locus control element, to the patic promoter and 5' to the polyadenylation signal (see AAI71003-16). The hepatic locus control element confers copy number dependent, position	BP. hepatic locus control element. tic locus control element; human; Pactor IX; blood clotting; gene therapy; ds.	are vectors that include an expression cassette of the invention. These may episomal or integrating vectors, including viral vectors, and are used in a claimed method of ameliorating the symptoms of a disease. A therapeutic amount of blood clotting Pactor IX is produced in mammalian liver cells for at least 100, and preferably at least 500, days. In examples of the invention, human Pactor IX was expressed in mouse liver cells following injection of retrovirus-based plasmids that carried the expression cassettes into the tail vein or portal vein, and by direct injection of plasmid DNA into the liver sequence 154 BP; 40 A; 47 C; 36 G; 31 T; 0 U; 0 Other; t Local Similarity 100.0%; Score 154; DB 6; Length 154; t Local Similarity 100.0%; Pred. No. 7.1e-40; t Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0; d GTTTGTGTGCTGCCTCTGAAGTCCACACTGAAACTTCAGCCTACTGTGCCTGAAA 60 
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, , , , , , , , , , , , , , , , , , ,	SULT 3 IT1005 AAI710 AAI710 18-MAR Human Apolip expres Homo s W02001 27-DEC 19-JUN 20-JUN	<pre>1 independent gene expression. Also provided are vectors that include an expression cassette of the invention. They are used in a claimed method of ameliorating the symptoms of a disease. A therapeutic amount of blood clotting Factor IX is produced in mammalian liver cells for a period of at least 100 days, and preferably at least 500 days. In examples of the invention, human Factor IX was expressed in mouse liver cells for a period of into the tail vein or portal vein, and by direct injection of plasmid DNA into the liver Sequence 328 BP; 72 A; 104 C; 84 G; 68 T; 0 U; 0 Other; Ouery Match Best Local Similarity 100.0%; Score 154; DB 6; Length 328; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 GTTTGTGTGTGTGCTGCTGCAAGTCCAAAGTCCAAACATCAAGCCTAACTCAAGTCCAAGTCCAAGCTGAAACATTCAAGCCTAACATCAAGCCTAACATCAAGCCTACTCATGTCCCTAAA 137 61 ATGGGCAAACATTGCAAGGTCCAAAGTCCAAACACAACACACAC</pre>

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nuce ms, Lichardon and particular and particular and particular approximation of a sequence for liver spectrific control as used for the provide and is used for the provide for the provide for the provide to the human hepatocyte-spectrol was operably linked to a promoth was operably linked to a transpirat the the construction of a transpirat afamin, the expression of the provide to the transpirate afamin.	<pre>XX 19-DEC-1995 (first entry) XX Human hepatocyte-specific control region. XX Human hepatocyte-specific control region; human afamin; HCR enhancer; XX promoter; transgene; transgenic animal; XX Homo sapiens. XX W09511308-A1. XX W09511308-A1. XX 13-OCT-1994; 94WO-US011675. XX 13-OCT-1994; 93US-00141322. PR 13-OCT-1994; 94WO-US011675. XX AMGE-) AMGEN, INC. XX Simpnet WS, Lichenstein HS, Lyons DE: XX</pre>	hepatic locus co pendent gene exp ession cassette ession cassette ors, including the syn thorating factor IX in ention, human Pace ethe liver the tail vein o the liver 1 GTTTGTGTGGGCI 1 GTTTGTGTGGGGCI 1 GTTTGTGTGGGGC 61 ATGGGCAAACA 61 ATGGGCAAACA 121 GGAGCTGGGGC 121 GGAGCTGGGGCC 121 GGAGCTGGGGCC 123 GGAGCTGGGGCC 124 GGAGCTGGGGCC 126 Btandard; D
88888888888888	9972922922292929229229229229229229229229	SXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
	<pre>Homo sapiens. WO200190419-A2. 29-NOV-2001. 23-MAY-2001; 2001WO-US016577. 23-MAY-2000; 2000US-02667938. 25-OCT-2000; 2000US-00697028. (VARI-) VARIAGENICS INC. (VARI-) VARIAGENICS INC. (STANY) STANTON V P. Stanton VP; WPI; 2002-097670/13. Determining the haplotype of at least one allele of a selected gene at two or more polymorphic sites, for assessing disease risk, comprises two or more polymorphic sites, for assessing disease risk, comprises </pre>	hepatic locus control element confers copy number dependent, position pendent gene expression. Also provided are vectors that include an ression cassette of the invention. These may epidomal or integrating tors, including viral vectors, They are used in a claimed method of locating the symptoms of a disease. A therapeutic amount of blood tring Factor IX is produced in mammalian liver cells for a period of east 100 days, and preferably at least 500 days. In examples of the factor of retrovirus-based plasnids carrying the expression cassettes ection of retrovirus-based plasnids carrying the expression cassettes the tail ver 100.0%; Score 154; DB 6; Length 771; east Similarity 100.0%; Score 154; DB 6; Length 771; iatch 100.0%; Score 154; DB 6; Length 771; iat 154; Conservative 0; Wismatches 0; Indels 0; Gaps 0; 1 STRIGTORGETGECTECTAAAGTECAAAAACTTCAAGETACTCATGTECTTAAA 60 

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Pr Delivering a protein to a mammal, useful in gene transfer, comprises pr contacting recombinant adeno-associated virus virions free of helper virus and having heterologous gene encoding a protein, with a duct of a pr secretory gland of mammal. XX PS Example 1; Page 32; 48pp; English. XX The invention relates to delivering a protein to a mammal that involves CC contacting recombinant adeno-associated virus (rAAV) virions, which are CC free of helper virus, and comprises heterologous gene encoding a protein, CC with a duct of a secretory gland of mammal resulting in the transduction CC heterologous gene is useful in the manufacture of a medicament for the eral gene is useful in the manufacture of a medicament for treating protein may also be used in the manufacture of a medicament for treating CC haemophilia. The method is useful in gene transfer, and to facilitate	PN W0200271843-A1. XX PD 19-SEP-2002. XX PF 14-MAR-2002; 2002WO-US008350. XX PF 14-MAR-2001; 2001US-0275908P. XX PA (AVIG-) AVIGEN INC. XX PT Mcclelland A, Scolley R; XX WEI; 2002-698779/75.	Qy       121 GGAGCTGGGGGAGAGGTCAGAGACCTCTCGGGC 154 	CC haplotype information can be used to make diagnostic tests useful for CC outcome of a disease, to diagnose a disease or condition, or to select an CC optimal therapy for a disease or condition. ABL31915 to ABL32035 CC represent nucleotide sequence used in the exemplification of the present XX SQ Sequence 1079 BP; 247 A; 284 C; 286 G; 262 T; 0 U; 0 Other; Dest Local Similarity 100.0%; Score 154; DB 6; Length 1079; Best Local Similarity 100.0%; Pred. No. 1.4e-39; Matches 154; CONSErVative 0; Mismatches 0; Indels 0; Gaps 0; 1 [[[1][1][1][1][1][1][1][1][1][1][1][1][1
<pre>YA (CHIK ) CHIKON COKF. XX Jolly DJ, Barber JR, Chang SMW, Respess JG, Allen JR, Boder M; PI Jolng K, De La Vega D, Depolo NJ, Hsu DC, Ibanez CB; PI Mittelstaedt DM, Prussak CE, Greengard J, Lee R; XX MPI; 1998-086966/08. XX PT New replication defective recombinant retro-viruses - which can be PT administered to provide long term systemic expression of therapeutic pT protein in blood, useful in, e.g. treating hyper-coagulable disorders. XX PS Example 33; Page 178; 272pp; English. XX CC This primer is used for generating the apolipoprotein B (Apo E) enhancer CC sequence. This is used to construct a retroviral vector backbone with a CC replication defective recombinant retrovirus (RRV) expressing a</pre>	Synthe Homo & WO980( 08-JA) 02-JUJ 02-JUJ 03-JUJ 13-AU( 13-AU( 13-AU(	<pre>RESULT 7 AAV19597 ID AAV19597 standard; DNA; 90 BP. XX AC AAV19597; XX AC AAV19597; XX DT 25-MAR-2003 (revised) DT 06-AUG-1998 (first entry) XX DE Apolipoprotein E (Apo E) enhancer sequence generating sense primer 3. XX Replication defective; recombinant retrovirus; RRV; therapeutic protein; XW Haemophilia; thrombosis; hypercoagulable disorder; liver disease; XW hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human; XW diabetes; hypopituitarism; adenine deaminase deficiency; HiV infection; XW anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease; XW enhancer sequence; PCR primer; ss.</pre>	CC pharmaco- or toxico-kinetic studies. The present sequence represents an CC apolipoprotein B (ApoB) locus control region nucleotide sequence XX SQ Sequence 154 BP; 40 A; 47 C; 35 G; 32 T; 0 U; 0 Other; Ouery Match 98.1%; Score 151; DB 6; Length 154; Best Local Similarity 100.0%; Pred. No. 6.7e-39; Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Db 4 GTITGTGTGCTGCTCTGAAGTCCACACTGAACATACTTCAGCCTACTCATGTCCCTAAA 60 

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Jolly DJ, Barber JR, Chong K, De La Vega D Mittelstaedt DM, Prus	(CHIR ) CHIRON CORP.		: 966T-1112-E0	PP 02-JUL-1997; 97WO-US011784.		OS Synthetic. OS Homo sapiens.		<pre>KW Replication defective; recomb KW haemophilia; thrombosis; hype KW hepatitis; thalassemia; pheny KW cystic fibrosis; Duchenne's M KW diabetes; hypopituitarism; ad KW anaemia; Gaucher's Syndrome; KW anaemia; Gaucher's Gaucher's Anaemia; Manaemia; Man</pre>		AAV19593;	RESULT 8 JAV19593 ID AAV19593 standard; DNA; 90 BP	DD 69 ÁTGGGCÁAÁCÁTTGCAAGCAGC	OY 61 ATGGGCAAACATTGCAAGCAGC	Oy         1         GTTIGTGIGCIGCCICTGAAGIC	Query Match 53.2%; S Best Local Similarity 100.0%; Matches 82; Conservative 0;	XX SQ Sequence 90 BP; 25 A; 25 C; 17	CC surviving inactivation in hum CC transfer over prolonged perio CC correct PI field.)	CC deficiency, Guacher a syndrom CC infection, high blood pressur CC inflammatory disease or graft	CC Dystrophy, inherited emphysem CC hypopituitarism, adenine deam	CC such as thalasemia, phenylke CC combined immunodeficiency (SC	CC preparation. The RRV's can be CC protein to treat, e.g. haemop CC hypercoagulable disorders. 11	CC The long term systemic expres CC therapeutic protein being pro CC of at least 30 days after the	CC therapeutic protein. The RRV CC human complement and is capab CC of the therapeutic protein wh	Mon Apr 24 07:43:10 2006
Chang SMW, Respess JG, Allen JR, Boder M; , Depolo NJ, Hsu DC, Ibanez CE; :mak CE, Greengard J, Lee R;				• •			, 88.	Replication defective; recombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholssterolemi; diabetes; hypopituitarism; adenine deaminase deficiency, HIV infection; anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease; anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease;	at entry) (Apo B) enhancer sequence generating sense primer 1.			GC 90	GC 82	GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60 	Score HZ; DH Z; Length Y0; Pred. No. 1.4e-16; Mismatches 0; Indels 0; Gaps 0;	7 G; 23 T; 0 U; 0 Other;	CC surviving inactivation in human serum thereby allowing efficient gene CC transfer over prolonged periods of time. (Updated on 25-MAR-2003 to CC correct PI field.)	yersus host disease. RRV's are capable of	a, tamiliai nypercnolescerolemia, diadeces, inase deficiency, alphal-antitrypsin a maamia infections such as HTV	Lonuria, Lesch-Nyhan syndrome, severe ID), cystic fibrosis, Duchenne's Muscular	used for in vivo delivery of therapeutic hilia A, haemophilia B, thrombosis, ver diseases such as hepatitis, disorders .	sion results in a measurable level of the duced in the blood of the human for a period administration of the RRV vector	and is capable of inducing long term systemic expression by and is capable of inducing long term systemic expression	)6 us-09-884-901a-8.rng
PR 03-JUL-1996; 96US-00645601. PR 13-AUG-1996; 96US-00696381. PR 04-JUN-1997; 97US-00869309.	02-JUL-1997;	XX PD 08-JAN-1998. XX	XX PN WO9800542-A2.	OS Synthetic. OS Homo sapiens.	<pre>KW Gene therapy; retrovirus; vector; apolipoprotein &amp;; Apox; ennancer; KW human; interferon; ss. XX</pre>	ApoE enhancer sense oligonucleotide.	20-JU	RESULT 9 AAV15382 ID AAV15382 standard; DNA; 90 BP. XX AC AAV15382;	QY     61 ATGGGCAAACATTGCAAGCAGC     82       Db     69 ATGGGCAAACATTGCAAGCAGC     90	QY       1 GTTTGTGTGCTCCTCTGAAGTCCACGCTGAACAACTTCAGCCTACTCALUCTCALUATER         Db       9 GTTTGTGTGCTCCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATCACCCTAAA         Bb       9 GTTTGTGTGCTCCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATCTCCCTAAA	Query Match 53.2%; Score 82; DB 2; Length 90; Best Local Similarity 100.0%; Pred. No. 1.4e-16; Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Sequence 90 BP; 24 A; 25 C; 18 G; 23 T;	CC transfer over prolonged periods of time. (Updated on 25-max-2005 co CC correct PI field.)	CC deficiency, Guacher's syndrome, anaema, intercutous such as the CC infection, high blood pressure, Alzheimer's disease, autoimmune or CC inflammatory disease or graft versus host disease. RRV's are capable of CC surviving inactivation in human serum thereby allowing efficient gene	CC combined immundeficiency (SCID), cystic fibrosis, Duchenne's Muscular CC Dystrophy, inherited emphysema, familial hypercholesterolemia, diabetes, CC hypopituitarism, adenine deaminase deficiency, alphal-antitrypsin CC hypopituitarism, adenine deaminase deficiency, alphal-antitrypsin	CC protein to treat, e.g. haemophilia A, haemophilia B, thrombosis, CC hypercoagulable disorders, liver diseases such as hepatitis, disorders CC such as thelassemia, phenylketonuria, Lesch-Nyhan syndrome, severe	CC The long term systemate expression results a more than for a period CC therapeutic protein being produced in the blood of the human for a period CC of at least 30 days after the administration of the RRV vector CC preparation. The RRV's can be used for in vivo delivery of therapeutic	CC human complement and is capable of inducing long term systemic expression CC of the therapeutic protein when administered intravenously to a human. CC of the therapeutic protein when administered intravenously to a human.	replication defective recombinant retrovirus (RRV) expressing a therapeutic protein. The RRV preparation is resistant to degrad	CC This primer is used for generating the appropriation is the sector of	Example 33; Page 177; 272pp; English.	PT administered to provide long term systemic expression of therapeutic PT administered to provide long term systemic expression of therapeutic PT protein in blood, useful in, e.g. treating hyper-coagulable disorders.		.a-8.rng raye J

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<pre>PI Jolly DJ, Barber JR, Chang SM, Respess JG, Allen JR, Boder M; PI Chong K, De La Vega D, Depolo NJ, Hsu DC, Ibanez CE; PI Mittelstaedt DM, Prussak CE, Greengard J; XX DR WPI; 1998-086967/08.</pre>	<pre>uman factor IX for the treatme assette was generated from a s issghorylated at the span the entire he gene strand and contains a tre was used, together with a to control expression of sorrs. The invention relates t uch as replication-defective gene therapy of genetic diseas r; O U; O Other; ; DB 2; Length 90; o. 1.4e-16; ches 0; Indels 0; Gap rGAACAAACTTCAGCCTACTCATGTCCCTA []] ]                                 </pre>	(CHIR ) CHIRON CORP. Jolly DJ, Barber JR, Chang SM, Respess JG, Allen JR, E Chong K, De La Vega D, Depolo NJ, Hsu DC, Ibanez CE; Mittelstaedt DM, Prussak CE, Greengard J; WPI; 1998-086967/08.
PS Example 33; SEQ ID NO 65; 138pp; English. XX CC The present invention provides methods for obtaining measurable levels of CC a protein, nucleic acid molecule or enzymatic product in a bodily fluid CC or cells of a human. The method involves administering to a human a	<pre>first oilgonuc_located havissie is for some error and and constains as' constained sharper constructive sourced, together with a live' construction relates for any settoring vectors. The invention relates to new recombinant gene dailyery vehicles, useh as replication-defective construction vectors, and their use in gene therapy of genetic diseases genetic docal similarity 51.3%; Score 82; DB 2; Length 90; Beet Local similarity 100.0%; Pred. No. 1.44-15; Natches 82; Conservative 0; Numatches 0; Indels 0; Gaps 0; 9 (1) CONSTRUCTOCTOCALCTICALACTICALACTICALCTICALTICUTION 0 (1) CONSTRUCTOCTOCALCTICALACTICALACTICALCTICALTICUTION 0 (2) (2) (2) (2) (2) (2) (2) (2) (2) (2)</pre>	<pre>XX PT New replication defective recombinant retroviruses - which express B PT domain-deleted human factor VIII or human factor IX for the treatment of PT haemophilia. XX PS Example 31; Page 146; 236pp; English. XX As apolipoprotein E (ApoE) enhancer cassette was generated from a set of CC As multipoprotein E (ApoE) enhancer cassette was generated from a set of CC As multipoprotein E (ApoE) enhancer cassette was generated from a set of CC As multipoprotein E (ApoE) enhancer cassette was generated from a set of CC As multipoprotein E (ApoE) enhancer cassette was generated from a set of CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette was generated from the entire CC As multipoprotein E (ApoE) enhancer cassette block the E (Contex E) enhancer cassette block the E (Contex E) enhancer cassette block the E (Contex E) enhancer enhance</pre>

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8888888	XX X X X X	XPPXP	X PR PR X PR			6 6 6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	888888888888888888888888888888888888888
Example 33; SEQ 1D NO 61; 13600; ENGLIEN. DR The present invention provides methods for obtaining measurable levels of a protein, nucleic acid molecule or enzymatic product in a bodily fluid or cells of a human. The method involves administering to a human a recombinant retroviral preparation having a titer on HT1080 cells of greater than 10 5 cfu/ml where the recombinant retroviral preparation is XX A protein, nucleic acid molecule or enzymatic product in a bodily fluid PT A protein, nucleic acid molecule or enzymatic product in a bodily fluid PT A protein fluid a protect of the protect	04-793566/78. h titre TK-1 retroviral vector expressing a factor VIII protein, in preparing a composition for treating hemophilia or thrombosis.		1997; 97US-00001039. 1994; 94US-00367071. 1996; 96US-00645601. 1996; 96US-00645601. 1997; 97US-0064501. 1997; 97US-00869381.	27-JAN-2005 (first entry)       DB         01igonucleotide #1 used to generate ApoB enhancer cassette.       XX         Haemophilia; thrombosis; gene therapy; haemostatic; thrombolytic;       XW         thymidine kinase; TK; ss; apolipoprotein B; Apo B.       XW         Unidentified.       XW         US6818439-B1.       XW         XX       XW <t< td=""><td>GGGCAAACATTGCAAGCAGC 90 andard; DNA; 90 BP.</td><td>5</td><td>recombinant retroviral preparation having a titer on HT1080 cells of greater than 10 5 cfu/ml where the recombinant retroviral preparation is capable of directing the expression of a protein, nucleic acid molecule or enzyme which generates an enzymatic product such that measurable levels of the protein, nucleic acid molecule or enzymatic product may be obtained in the bodily fluid or cells of the human. The invention also relates to a novel TK (thymidine kinase)-1 retroviral vector which expresses a factor VIII protein. The TK-1 retroviral vector is useful in preparing a composition for treating haemophilia, thrombosis and other disorders. The invention is useful in gene therapy. The present sequence is an oligonucleotide used to generate applipoprotein B (App B) enhancer</td></t<>	GGGCAAACATTGCAAGCAGC 90 andard; DNA; 90 BP.	5	recombinant retroviral preparation having a titer on HT1080 cells of greater than 10 5 cfu/ml where the recombinant retroviral preparation is capable of directing the expression of a protein, nucleic acid molecule or enzyme which generates an enzymatic product such that measurable levels of the protein, nucleic acid molecule or enzymatic product may be obtained in the bodily fluid or cells of the human. The invention also relates to a novel TK (thymidine kinase)-1 retroviral vector which expresses a factor VIII protein. The TK-1 retroviral vector is useful in preparing a composition for treating haemophilia, thrombosis and other disorders. The invention is useful in gene therapy. The present sequence is an oligonucleotide used to generate applipoprotein B (App B) enhancer
<b>WPI;</b> 1998-086966/08. <b>R</b> <b>P</b> <b>New replication defective recombinant retro-viruses - which can be <b>P</b> <b>P</b> <b>Administered to provide long term systemic expression of therapeutic <b>P</b> <b>P</b> <b>P</b> <b>P</b> <b>P</b> <b>P</b> <b>P</b> <b>P</b></b></b>	Jolly DJ Chong K, Mittelst		S Synthetic. Homo sapiens. WO9800541-A2. C 08-JAN-1998. C 02-JUL-1997; 97WO-US011784.	Apolipoprotein E (Apo E) enhancer sequence generating antisense primer 3. Replication defective; recombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi; anaemia; Gaucher's syndrome; high blood pressure; Alzheimer's disease; autoimmune; inflammatory disease; adenovirus 2; Apolipoprotein E; Apo E; enhancer sequence; PCR primer; SB.	SULT 13 V19599/c AAV19599 standard; DNA; 82 BP. AAV19599; 25-WAR-2003 (revised) 06-AUG-1998 (first entry)	Sequer Sequery Mat Best Loca Matches	

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XX DR WPI; 2004-793566/78.	Jolly DJ, Char Greengard J, 1	(CHIR ) CHIRON	PR 30-DEC-1994; 94US-00367071. PR 03-JUL-1996; 96US-00645601. PR 13-AUG-1996; 96US-00695381. PR 04-JUN-1997; 97US-00869309.	30-DEC-1997;		27-JAN-2005 (first entry) Oligonucleotide #7 used to	AC ADU47589; XX	RESULT 14 ADU47589/c ID ADU47589 standard; DNA; 82 BP.	Oy         135         GGTCAGAGACCTCTCTGG         152           Db         22         GGTCAGAGACCTCTCTGG         5	Db 82 CAAGCAAGCAAACAGCAAACACAG	75	Query Match 50.6%; Sc Best Local Similarity 100.0%; P Matches 78; Conservative 0;	Sequence 82 BP; 13 A; 21 C; 26	CC inflammatory disease or graft v CC surviving inactivation in human CC transfer over prolonged periods CC correct PI field.) XX	deficiency, Guacher's	CC combined immunodeficiency (SCID CC Dystrophy, inherited emphysema, CC hypophysical advanta	CC hypercoagulable disorders, live CC such as thalassemia, phenylketo	CC preparation. The RRV's can be u CC protein to treat, e.g. haemophi	CC therapeutic protein being produ CC of at least 30 days after the a	CC of the therapeutic protein when CC The long term systemic expressi	CC therapeutic protein. The RRV pr CC human complement and is capable	CC liver specific promoter. The in CC replication defective recombina	CC This primer is used for generating CC sequence. This is used to construct	<b>EXample 33; Page 178; 272pp;</b>
	Depolo NJ, Hsu DC, Ibanez CE;					generate ApoE enhancer cassette.				HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GCCTGCTGACCTTGGAGCTGG	Score 78; DB 2; Length 82; Pred. No. 2.7e-15; '' Mismatches 0; Indels 0; Gang 0;	G; 22 T; 0 U; 0 Other;	RV'S are cap ng efficient 25-MAR-2003	anaemia, infections such as HIV Alzheimer's disease, autoimmune or	iency (SCID), cystic fibrosis, Duchenne's Muscular emphysema, familial hypercholesterolemia, diabetes,	r diseases such as hepatitis, disorders nuria, Lesch-Nyhan syndrome, severe	sed for in vivo delivery of therapeutic lia A, haemophilia B, thrombosis,	ced in the blood of the human for a period ininistration of the RRV vector	administered intravenously to a human. on results in a measurable level of the	eparation is resistant to degradation by of inducing long term systemic expression	paration of essing a	ing the apolipoprotein E (Apo E) enhancer ruct a retroviral vector backbone with a	kngilsn.
PA (CHIR) CHIRON CORP.	PR 03-JUL-1996; 96US-00645601. PR 13-AUG-1996; 96US-00696381. PR 04-JUN-1997; 97US-00869309.	PF 02-JUL-1997; 97WO-US011784. XX	WO98005 08-JAN-	Synthet Homo sa	KW Replication defective; recombinant retrovirus; RRV; therapeutic protein; KW haemophilia; thrombosis; hypercoagulable disorder; liver disease; KW hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; human; KW cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterclemi; KW diabetes; hypopituitarism; adenine deaminase deficiency, HIV infection;	Apolipoprotei	AA DT 25-MAR-2003 (revised) DT 66-AUG-1998 (first entry)	AAV19595/c ID AAV19595 standard; DNA; 82 BP. AC AAV19595; AC AAV19595;	Db 22 GGTCAGAGACCTCTCTGG 5	Qy 135 GGTCAGAGAGCCTCTCTGG 152		Hest Local Similarity 100.0%; Fred. No. 2./e-15; Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps Ov 75 CAAGCAGCAAACAGCAAACACAGCGCTGCCTGCCTGACCTTGGAGCTGGGGGGGG	50.6%; Score 78;	CC recombinant gene delivery vehicles for the treatment of haemophilia and CC other disorders. XX SQ Sequence 82 BP; 13 A; 21 C; 26 G; 22 T; 0 U; 0 Other;	CC discription of the used to generate apolipoprotein S (Apo E) enhancer CC cassette. This sequence is used in the method for administration of	expresses a factor VIII protein. The TK-1 retroviral vector is upreparing a composition for treating haemophilia, thrombosis and	CC obtained in the bodily fluid or cells of the human. The invention also CC relates to a novel TK (thymidine kinase)-1 retroviral vector which	CC or enzyme which generates an enzymatic product such that measurable CC levels of the protein, nucleic acid molecule or enzymatic product may be	CC greater than 10 5 cfu/ml where the recombinant retroviral preparation is	CC or cells of a human. The method involves administering to a human a CC recombinant retroviral preparation having a titer on HT1080 cells of	CC The present invention provides methods for obtaining measurable levels c CC a protein, nucleic acid molecule or enzymatic product in a bodily fluid	Example 33; SEQ ID NO 67; 138pp; English.		New hi

The present invention provides methods for obtaining measurable levels of a protein, nucleic acid molecule or enzymatic product in a bodily fluid or cells of a human. The method involves administering to a human a recombinant retroviral preparation having a titer on HT1080 cells of greater than 10 5 cfu/ml where the recombinant retroviral preparation is capable of directing the expression of a product such that measurable or enzyme which generates an enzymatic product such that measurable levels of the protein, nucleic acid molecule or enzymatic product may be obtained in the bodily fluid or cells of the human. The invention also relates to a novel TK (thymidine kinase)-1 retroviral vector which expresses a factor VII protein. The TK-1 retroviral vector is useful in preparing a composition for treating haemophila, thrombosis and other disorders. The invention is useful in gene therapy. The present sequence is an oligonucleotide used to generate apolipoprotein E (hpo B) enhancer cassette. This sequence is used in the method for administration of networdered. 9595; R-2003 (revised) G-1998 (first entry) IC CD nce 82 BP; 13 A; 21 C; 26 G; 22 T; 0 U; 0 Other; ple 33; SEQ ID NO 67; 138pp; English. poprotein E (Apo E) enhancer sequence generating antisense primer 1. al Similarity 595 standard; DNA; 82 BP. 135 GGTCAGAGACCTCTCTGG 152 22 GGTCAGAGACCTCTCTGG 5 disorders. 78; Conservative 50.6%; Score 78; DB 13; Length 82; 100.0%; Pred. No. 2.7e-15; <u>,</u> Mismatches 2.7e-15; hes 0; Indels

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CHIRON CORP.

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Jolly DJ, Barber JR, Chang SMW, Respess JG, Allen JR, Chong K, De La Vega D, Depolo NJ, Hsu DC, Ibanez CE; Mittelstaedt DM, Prussak CE, Greengard J, Lee R; Boder M;

WPI; 1998-086966/08.

New replication defective recombinant retro-viruses - which can be administered to provide long term systemic expression of therapeutic protein in blood, useful in, e.g. treating hyper-coagulable disorders.

Example 33; Page 177; 272pp; English.

therapeutic protein. The RRV proparation is resistant to degradation by therapeutic protein. The RRV proparation is resistant to degradation by therapeutic protein when administered intravenously to a human. the long term systemic expression results in a measurable level of the therapeutic protein being produced in the blood of the human for a period of at least 30 days after the administration of the RRV vector proparation. The RRV's can be used for in vivo delivery of therapeutic protein to treat, e.g. haemophilia A, haemophilia B, thrombosis, cc protein to treat, e.g. haemophilia A, haemophilia B, thrombosis, cc such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe cc combined immundeficiency (SCID), cystic fibrosis, Duchenne's Muscular cc hypopituitarism, adenine deeminase deficiency, alphal-antitrypsin cc infaction, high blood pressure, Alzheimer's disease, autoimmune or infaction, high blood pressure, Alzheimer's disease, autoimmune of surving inactivation in human serum thereby allowing efficient gene transfer over prolonged periods of time. (Updated on 25-MAR-2003 to correct PI field.) This primer is used for generating the apolipoprotein E (Apo E) enhancer sequence. This is used to construct a retroviral vector backbone with a liver specific promoter. The invention provides the preparation of replication defective recombinant retrovirus (RRV) expressing a

Sequence 82 BP; 12 A; 21 C; 27 G; 22 T; 0 U; 0 Other;

Query Match Best Local S Matches 77 77; Similarity 50.0%; Score 77; DB.2; Le ilarity 100.0%; Pred. No. 5.8e-15; Conservative 0; Mismatches 0; Length 82; Indels <u>,</u> Gaps

<u>,</u>

Ş 75 CAAGCAGCAAACAGCAAACACACACACCCTCCCTCCCTGCTGCACCTTGGAGCTGGGGCAGA 134

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Search completed: April 18, 2006, 13:22:04 Job time : 95.4261 весв

C       1       38       24.7       958       10       CNS0044W       AL06467       Drosophil         C       2       3.5.6       23.1       5.43       1       AL279008       AU279008       AU279008         C       3       35.6       23.1       6.43       1       AU279008       AU279008       AU279008         C       4       35.4       23.0       469       B       CX307208       CX307208       CX307208       CX307208       AU279008       AU27908       AU279	of results predicted by chance to have nual to the score of the result being pr is of the total score distribution. SUMMARIES B ID Descriptio	Database : EST:* 1: gb_est1:* 2: gb_est2:* 3: gb_est2:* 4: gb_htc:* 5: gb_est4:* 6: gb_est4:* 9: gb_est5:* 9: gb_est5:* 10: gb_gss2:* 11: gb_gss3:*	Maximum DB seq length: 200000000° Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Gapop 1 1: 4107832 umber of hits sa	Title: US-09-884-901A-8 Perfect scoré: 154 Sequence: 1 gtttgtgtgctgcctctgaaggtcagagacctctctgggc 154 Section table. ThewTTTY NTC	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. OM nucleic - nucleic search, using sw model Run on: April 18, 2006, 12:18:29 ; Search time 747.823 Seconds (without alignments) 9634.919 Million cell updates/sec	Mon Apr 24 07:43:11 2006 us-09-884-901a-
please see http://www.fruitfly.org The BDCP Drosophila melanogaster genome Using trese bacs. very a sprepared by Kazutoyo Osoegawa and Aaron Mamoseer in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EscRI digestion of Drosophila DNA provided by the BDCP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's filters for hybridization from the BACRAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. I. 958 Bource // Mol_type="genomic DNA" /db_xref=tatxan:?2?" /clone_TBACR00023" /note="end : TET3"	REFERENCE 1 (bases 1 to 958) AUTHORS Genoscope. TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila formation	4W/C CNS0044W TION Drosophila mela BACR09M23 of RI ION AL066467 N AL066467.1 GI DS Drosophila mela NISM Drosophila mela NEW Drosophila mela Neoptera; Endop Bohydroidea; Dr	ALIGNMENTS	39 32.8 21.3 554 3 LASS4/4/ 41 32.8 21.3 583 10 AG973280 41 32.8 21.3 623 10 AG970743 42 32.8 21.3 1049 3 BM423372 43 32.4 21.0 467 3 BB614956 44 32.4 21.0 640 9 CE010717 45 32.4 21.0 752 7 CF951791	34 33.4 21.7 764 10 CL/12133 35 33.4 21.7 835 10 CL/26784 36 33.4 21.7 2775 10 CL965222 37 32.8 21.3 444 5 BY388939 38 32.8 21.3 477 9 AZ787078		-901a-8.rst Page 1

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Ş 밇 昂 Ş REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION RESULT 2 CB458659/c Ś ORIGIN FEATURES COMMENT 8 昂 Ş 昂 Ś KEYWORDS DEFINITION **S** D O C U S Matches 62; Query Match Best Local Similarity TITLE JOURNAL Query Match 24.7%; Best Local Similarity 38.9%; Matches 49; Conservative 29 source 112 TGCCCAGGAATTAAAAAAAAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC 564 122 624 52 11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAAATGGGCAAAC Tel: 402 762 4366 Fax: 402 762 4360 Email: smitheemail.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross match v0.99029 plate: FQY8072 row: D column: 12 Bos taurus (cow) Bos taurus Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Boyidae; Boyinae; Bos. Seq 1 (bases 1 to 329) Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W. A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003) EST. CB458659 329 bp mRNA linear 717364 MARC 6BOV Bos taurus cDNA 3', mRNA sequence. CB458659.1 GI:29265043 USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Contact: Smith TPL AATTTATTCAGAAGTGAAAAAAACAGTAAAGGAACCTGTCCTGCTG GAGMIG 559 GAGCTG 127 primer: Conservative /db\_xref="taxon:9913"
/tissue\_type="pooled"
/lab\_hogt="DH108"
/lab\_hogt="DH108"
/clone\_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site\_1: EcoRI; Site\_2: NotI;
Library made with RNA pooled From multiple tIssues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium." Y8072 row: D column: 12 r: TAGAAGGCACAGTCGAGG. Location/Qualifiers /organism="Bos taurus" /mol\_type="mRNA" .329 23.5%; 29; 0; Mismatches Score 36.2; DB 6; Pred. No. 5.5; Score 38; DB 10 Pred. No. 2; 19; Mismatches DB 10; Length 958; 43; Indels 48; Indels Length 329; 8 EST 26-MAR-2003 °, <u>,</u> Gaps Gaps ទួ 70 0 0 REI DEF SOLAC 昂 2 昂 Ş õ RE 周 8 ខ្លួងខ្ល BPS

RESULT 3

RESULT 5 CK779717/c ACCESSION VERSION 昂 Ś 皍 Ś 昂 Ś FEATURES COMMENT SOURCE ORIGIN COMMENT REFERENCE DEFINITION Pocus KEYWORDS JOURNAL PUBMED Query Match TITLB TITLE AUTHORS JOURNAL ORGANI SM Matches Best Local BOUTCE 149 368 308 TGAAGCAGCAGCTAACACTGCCTACAGGCCCGGCTGCGTGGCCAATAGTCGGAAAACCTTC 248 İGTATTCATİTGCGCGİAAİCAACİGTCCAAGAATAGAAGAAGCAGCGAGCAGAAAAACAA 307 29 TGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAACATTGCAAGCAGCAAACAG 88 89 CAAACACACAGGCCTCCCTGCCTGCTGACCTTGGAGCTGGGGGCAGAGGTCAGAGACCTCT 148 sequence. CK779717 ; 69 Development of a citrus genome-wide EST collection and cDNA microarray as resources for genomic studies Plant Mol. Biol. 57 (3), 375-391 (2005) Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C., Roberts,R.M., Smith,M.F. and Youngquist,R.S. USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female EST. CK779717 363 bp mRNA linear EST 23-FEB-2/ UMC-bend\_0B01-012-g01 Day 8 Uterus bend Bos taurus cDNA 3', mRNA Genomics Laboratory Instituto de Biología Molecular y Celular de Plantas (Universidad Polítecnica de Valencia - Consejo Superior de Investigaciones Contact: DNA Core Pacility (Bovine Project) Animal Science - RS Prather University of Missouri-Columbia M616 Medical Sciences Bldg., Columbia, MO 65212, USA Fax: Unpublished (2002) Reproduction Pecora; Bovidae; Bovinae; 1 (bases 1 to 363) Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammaliaː Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Bos taurus Bos taurus (cow) CK779717.1 GI:42745395 **Email**: Avenida Cientificas) Contact: Forment J 15830128 Similarity CAGAG 372 CTGGG 153 Conservative (573)884-5552 (573) 882-0428 i de los Naranjos s/n, jforment@ibmcp.upv.es bovine@rnet.missouri.edu /tlssue\_type="flavedo"
/dev\_stage="adult\_trees"
/lab\_host="Bscherichia\_coli"
/clone\_lib="PlavPrSub1"
/note="Organ: fruits; Vector: ] /note="Organ: fruits; Vector: pCR2.1; Subtracted cDNA library made from poly-A+ RNA from flavedo of fruits stored at 2oC for 14 days, subtracted with poly-A+ RNA from fruits stored at 12oC for 14 days" Location/Qualifiers organism="Citrus clementina x Citrus tangerina" 'mol\_type="mRNA" 'cultivar="Fortune" sex="hermaphrodite" clone="C19002D06" db\_xref="taxon:307631" .469 23.0%; <u>.</u> Score 35.4; Pred. No. 10; Mismatches Bog. 46022 Valencia, Spain DB 8; 56; Indels Length 469; 0 ;; 23-FEB-2004 Сарв , 367 0

thund at the following unit edu/Bovine/Methods.html. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Olagen) according to tissue(J1). Briefly, Imog of poly(A)+ RNA was annealed at C37 degrees with SuperScript II (Invitrogen, reverse transcriptese (Jiang et al., 2001). The 'Law annealed at tissue(Jasge-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonuclocitde used to prime first-etrand synthesis. Second strand synthesis was performed with Juage rehnologies) and digeters (Invitrogen, Ita CDNA were ligated to Sall adapters (Invitrogen VI and from each developmental stage of a particular tissue were selected by passage through toWA with singue were selected by passage through toWA with the converse transition the Notion (Invitrogen). After fisctionally into the Noti and Sall stage of the production with the standard protocol) The resource of the inserts the plasmids were electroporated into DHOB bacteria. Library Construction (PCR Protocol): The amount of mRNA that was recovered from portice and embryos was guite limiting and was not sufficient for library production with the standard protocol) Therefore, PCR-based protocol was utilized for producing libraries from sources in which the standard protocol) the SMAT oligonucleotide and a synAPT oligonucleotide by WAS syntexide to contain a sall site to generate full-length cDNA with a sequence complementary to the SMAT oligonucleotide. Sequences -source as (for the SMAT oligonucleotide sequence source of applify the cDNA by PCR with pfu turbo /clone lb="bend" /clone "Funding: The production of BSTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine BSTs: Focus on Female Reproduction' to RS Prather, B Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MP Smith and RS Youngquist. Genetic Source: Heifers for selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: ocytes; in vitro derived embryos (2-cell, morila, blastocyst and nuclear transfer blastocyst); in vivo blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early follicles (days 0, non-recruited, recruited, early at least 4 generations. Samp consisted of the following: MF Smith and RS Youngquist. Genetic Source: Heirers ior the project were purchased from Circle A Ranch, Iberia, (http://www.circlearanch.com/home.html). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples polymerase (Stratagene). The ₿ "mol\_type="mRNA" organism="Bos taurus" ocation/Qualifiers xref="taxon:9913" germinal vesicle-stage resulting PCR products were Iberia, MO

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JOURNAL Unpublished (2002) COMMENT Contact: DNA Core Pacility (Bovine Project) Animal Science - RS Prather University of Missouri-Columbia MO 65212. USA MG16 Medical Sciences Bldg. Columbia. MO 65212. USA	<pre>Butheria; Laurasiatheria; Cetartiodactyla yidae; Bovinae; Bos 1 to 401) S., Antoniou,E., Garverick,H.A., Green,J.? M., Smith,M.F. and Youngquist,R.S. MRI-2002-03476: Bovine ESTs: Focus on Fer on</pre>	ACCESSION C0727732 VERSION C0727732.1 GI:50710669 VERVORDS EST. SOURCE Bos taurus (cow) ORGANISM Bos taurus (cow) DRGANISM Bos taurus (cow) Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	RESULT 6 CO727732 LOCUS DEFINITION UMC-bend_0A02-023-b04 Uterus (endometium) bend Bos taurus CDNA 3', mRNA Asquence	Oy 71 ATTGCAAGCAGAAACAGCAAAACACAGGCCTGCCTGCCTG	Oy         11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAAATGGGCAAAC         70           IIII         IIIII         IIII         IIII         IIII         IIII         IIII         IIIII         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Query Match 22.9%; Score 35.2; DB 7; Length 363; Best Local Similarity 58.7%; Pred. No. 11; Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;	purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified CDNA from each PCR reaction was quantitated and mixed on an equimolar basis for lighting into the pCNV- SPORTS vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <4%), ribosomal RNA clones representing the gredominant clones in each library (mega-library) for more sequenced at the University of the library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests for clones should be made to the Director of the University of Missouri-Columbia. Clone Requests for clones should MF, Lennon G, Soares MB, Normalization and Subtraction if No approaches to facilitate gene discovery. Genome Res, 1956; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth MW, Green JA, Fortester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:394-2. Soares MB, MF Banaldo, P Jelene, L Su, Liawton, A Efetranitadis. 1994. Construction and characterization of a normalized cDNA library proc Natl Acad Sci, 91:928-9232. TAG_TISSUB=Day 8 Uterus
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DLYA=No. mail: S (573)882-0428 (573)884-5552 Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly (A) + RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with (GCTGCTGCGGCGCGC-tag-T18) and reverse transcribed at C37 degrees with SuperScript J1 (Invitrogen, cat. no. 18248-013). Briefly, Imcg of poly (A)+ RNA was anneailed at C37 degrees with SuperScript J1 (Invitrogen, cat. no. (http://genome.uiowa.edu/pubsoft/software.html) presents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) presents in After second strand synthesis, the double-strand synthesis. Were ligated to SalI adapters (Invitrogen). Life selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies) and digested with NotI. The cDNAs were size of developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the presents. the plasmid were electroporated into DH108 bacteria. Library Construction (PCR Protocol): The amount of mRNA that was bovine@rnet.missouri.edu recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PGR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroBoly (A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dT18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a blastocysts and conceptuses (days 8, 14, 16 and 18); corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL; at least 4 generations. Samples collected: The sample consisted of the following: germinal vesicle-stage ocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo B Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (http://www.circlearanch.com/home.html). These heifers, /note="Funding: The production of ESTs submitted in this project was funded by USDA Grant MRI-2002-03476 entitled 'Bovine ESTs: Pocus on Pemale Reproduction' to RS Prather, Sall site to generate full-length while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples http://genome.rnet.missouri.edu/Bovine/Methods.html Location/Qualifiers 'clone lib="bend" mol\_type="mRNA" db\_xref="taxon:9913" organism="Bos taurus" ŝ cDNA with a sequence

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RESULT 7 BF042501 LOCUS DEFINITION ACCESSION SUBJUCE SOURCE SOURCE ACCESSION BF042501.1 GI:10759556 SOURCE SOURCE ORGANISM Bos taurus Bos tauru	Db 112 TGCCCAGGAATTAAAAAAAAAAAAAAGCAACTTCAGCCTCCCCATCTCCAACAAAAAAAA		zed dis	<pre>(mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovin@ørnet.missouri.edu. Bonaldo MF, Lennon G, Soares MB, Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res. 1966; 6:791-806. Jiang H, Bivens NJ, Ries JE, Cenome Res. 1966; 6:791-806. Jiang H, Bivens NJ, Ries JE,</pre>	library quality (e.g. the presence of short polyA tails, genomic DNA contamination (must be cl*), ribosomal RNA clones (must be cl*), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library	complementary to the SMART oligonucleotide. Sequences within the SMART and dT oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV- spORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by memoring (-4 96-well plates) to confirm
ACCESSION AU279081.1 GI:21682391 VERSION AU279081.1 GI:21682391 SOURCE ORGANISM EST. SOURCE ORGANISM Est aurus (cow) DORGANISM Est aurus (cow) Mammalia, Eutheria, Chordata, Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Ruminantia; Pecora; Bovidae; Bovinae; Bos. 11 (bases 1 to 567) AUTHORS 0ishi, Yamada, T., Goma, H., Lejukole, H.Y., Taniguchi, Y. and Sasaki, Y. Sasaki, Y. TITLE Sasaki, Y. Gontact: Masahico Oishi Contact: Masahico Oishi Graduate School of Agriculture Kyoto University Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan Tel: 81-75-753-6331 Email: oishi@jkans.jkans.kais.kyoto-u.ac.jp.	RESULT 8 AU279081/c LOCUS DEFINITION AU279081 Cloned bovine placenta CDNA Bos taurus CDNA clone	OY       11 TECCTCTGAAGTCCACACTGAACATAACTTCAGCCTACTCATCTCCCTAAAATGGGCAAAC 70         Db       127 TECCCAGGAATTAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATAACAGAAAC 186         OY       71 ATTECAAGCAGCAACAACACACACACACCCTCCCCCCTGCCTGC	As described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. " ORIGIN Query Match Best Local Similarity 58.7%; Pred. No. 12; Matches 61; Conservative 0; Mismatches 43; Indels 0; Gaps 0;	<pre>source /organism="Bos taurus" /mol_type="mRNA" /db_xref="mRNA" /cloine="BP250012A10B5" /lab_nost=#P10B" /lab_nost=#H10B" /cloine_lib="Soares normalized bovine placenta" /cloine_lib="Soares normalized bovine placenta")</pre>		University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5998 Pax: 217 244 5617 Email: h-lewin@uluc.edu Funding for cattle EST sequencing was provided by the USDA National Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.

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(lab host="PHIOR HARC 6BOV"       (/lab host="PHARC 6BOV"         (clore_lib="WARC 6BOV"       (/loce1): EcoRI; Site_1: EcoRI; Site_2: NotI;         (hote="Vector: pcDNA1.1; Site_1: EcoRI; Site_2: NotI;       (/loce1): EcoRI; Site_1: EcoRI; Site_2: NotI;         (hote="Vector: pcDNA1.1; Site_1: EcoRI; Site_2: NotI;       (/loce1): EcoRI; Site_1: EcoRI; Site_2: NotI;         (hote="Vector: pcDNA1.1; Site_1: EcoRI; Site_2: NotI;       (/loce1): EcoRI; Site_1: EcoRI; Site_2: NotI;         (hote="Vector: pcDNA1.1; Site_1: EcoRI; Site_2: NotI;       (/loce1): EcoRI; Site_2: NotI;         (hote: pcdnath="docentary"): pcdnath="docentary", and placentary", and placentary       (/loce1): EcoRI; Site_2: NotI;         (placentary"): pcdnath="docentary", lung, hypothalamus, pituitary, and placentary       (/loce1): EcoRI; Site_2: NotI;         (placentary"): placentary       (/loce1): EcoRI; Site_2: NotI;       (/loce1): EcoRI; Site_2: NotI;         (placentary"): placentary       (/loce1): EcoRI; Site_2: NotI;       (/loce1): EcoRI; Site_2: NotI;         (placentary"): placentary       (/loce1): EcoRI; Site_2: NotI;       (/loce1): EcoRI;         (placentary"): placentary       (/loce1): EcoRI; Site_2: NotI;       (/loce1): EcoRI;         (placentary: placentary:	TITLE       A Becond set of Dovine ssis from pooled-fissue normalized libraties         JOURNAL       Unpublished (2003)         COMMENT       Contact: Smith TPL         USDA, ARS, US Meat Animal Research Center         pO Box 166, Clay Center, NE 68933-0166, USA         Tel: 402 762 4366         Fax: 402 762 4366         Email: smith@email.marc.usda.gov         Single pass sequencing. Bases called with phred v0.020425.c and         trimmed with the aid of the trim_alt option. Vector identified with         plate: F078034 row: P column: 15         Seq primer; GTAATAGGACTCATARAGGS         source       /organism="Bos taurus"         /obs refer taxon:9913"         /db xrefer taxon:9913"	10 10 4 4 CB434484 10N CB434484 CB434484 CB434484 CB434484 CB434484 CB434484 CB434484 CB434484 CCW Bos taurus (cow) ISM Bos taurus (cow) ISM Bos taurus (cow) ISM Bos taurus (cow) ISM Bos taurus (cow) ISM Bos taurus (cow) Sukaryota; Metazoa; Chordata; Craniata; Vertebs Bukaryota; Metazoa; Chordata; Craniata; Vertebs Bukaryota; Metazoa; Chordata; Craniata; Vertebs Sukaryota; Metazoa; Chordata; Craniata; Vertebs Mammalia; Butheria; Laurasiatheria; Cetartioda Pecora; Bovidae; Bovinae; Bos. CB 10 (bases 1 to 615) RS Mray, J.E. and Keele; J.W.	GACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC 70                               AAAGCAACTTCAGCCTCCCCATCTCAACAAATACAGAAAC 19 AAACACACAGGCCCTCCCCGCTGCT 114                         AAACAGTAAAGGAACCTGTCCTGCT 239	Soares laboratory and it was constructed and no as described by Bonaldo, M.F., Lennon, G. and S M.B. (1996), Genome Research 6(9): 791-806. " atch 22.9%; Score 35.2; DB 2; Length 579; cal Similarity 58.7%; Pred. No. 13; cal Similarity 58.7%; Pred. No. 13;

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SOURCE REFERENCE AUTHORS REFERENCE AUTHORS SOURCE ORGANISM Ş 뎡 Ş COMMENT 昂 ORIGIN FEATURES KEYWORDS VERSION ACCESSION DEFINITION CB457803 DEFINITION БCGS **RESULT 11** VERSION ACCESSION LOCUS CK970120 RESULT 12 **CEYWORDS** Matches Query Match TITLE Best Local Similarity JOURNAL TITLE BOUTCE 137 11 71 77 61; sequence. CK970120 cross\_match v0.990329. Plate: FQY8073 row: C column: 5 Seq primer: GTAATACGACTCACTATAGGG. A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003) Contact: Smith TPL 1 (bases 1 to 716) Smith, T. P. L., Roberts, A. Wray, J. B. and Keele, J.W. CB457803.1 GI:29264185 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with Bukaryota; Metazoa; Mammalia; Butheria; Bos taurus EST CB457803 716 715917 MARC 6BOV Bos taurus Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gabarre, L.C. Production of EST from cDNA libraries derived from immunologica activated bovine gut Bos taurus (cow) Bos taurus EST CK970120.1 GI:45488094 4085432 BARC Email: smith@email.marc.usda.gov Tel: 402 762 4366 Fax: 402 762 4390 USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Pecora; Bovidae; Bos taurus CK970120 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. 1 (bases 1 to 732) TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC AATTTATTCAGAAGTGAAAAAAACAGTAAAGGAACCTGTCCTGCT 180 TGCCCAGGAATTAAAAAAAAAAGCAACTTCAGCCTCCCCCATCTCCAACAAAATACAGAAAC Conservative /note="Vector: pcDUA3.1; Site 1: EcoRI; Site 2: Noti; /note="Vector: pcDUA3.1; Site 1: EcoRI; Site 2: Noti; Library made with RNA pooled From multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium." location/Qualifiers clone 'lab\_host="DH10B" db\_xref="taxon:9913" mol\_type="mRNA" organism="Bos taurus" (cow) .716 9BOV 22.9%; Roberts, A.J., Bchternkamp, S.B., lib="MARC 6BOV" Bovinae; Bos. Bos taurus Chordata; Craniata; Vertebrata; Euteleostomi; Laurasiatheria; Cetartiodactyla; Ruminantia; <u>,</u> Score 35.2; D) Pred. No. 13; 0; Mismatches 716 bp 732 cDNA 5', mRNA sequence. bp mRNA cDNA clone mRNA B 43; 6; linear EST 15 9BOV2\_A09 5', mRNA Length linear Indels Chitko-McKown, C.G., L.C. from immunologically 716; EST 16-MAR-2004 EST 26-MAR-2003 <u>,</u> Gaps 136 70 <u>,</u> RESULT 13 CK834244 COMMENT VERSION KEYWORDS LOCUS 昂 Ś 昂 Ş ORIGIN FEATURES COMMENT REFERENCE SOURCE ACCESSION DEFINITION JOURNAL Matches Best Local Similarity Query Match ORGANISM TITLE JOURNAL AUTHORS Bource 147 87 Tel: 3015048604 Fax: 3015048744 Email: rbaumann@ 71 H sequence. CK834244 61; Contact: Tad S. Sonstegard Bovine Functional Genomics Laboratory Animal and Natural Resources Institute Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 742)
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassell,C.P. EST. CK834244 742 bp mRNA linear EST 04 4058470 BARC 8BOV Bos taurus cDNA clone 8BOV\_2D12 5', mRNA by cross match using options -minmatch Plate: 2 row: A column: 09 Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim\_alt " -trim\_fasta. Vector ident Unpublished (2004) Intestinal Muscle and Unpublished (2004) Contact: Richard G. Ba Bos taurus High Seq primer: CCCAGTCACGACGTTGTAAAACG Email: tads@anri.barc.usda.gov Fax: 3015048414 Tel: 3015048416 Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle Bos taurus (cow) CK834244.1 Single BLDG 162: BARC-EAST, ANRI Bovine Functional Matukumalli,L.K. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; TECCTCTERARETCCACACTERARCAAACTTCAECCTACTCATETCCCTAAAAATGGGGCAAAC AATTTATTCAGAAGTGAAAAAAAAAGGAAGCTGTCCTGCT 22.9%; nilarity 58.7%; Conservative quality sequence stop: 732. Location/Qualifiers pass rbaumann@anri.barc.usda.gov pass sequencing. Bases called /mol\_type="mRNA" /strain="Holstein" /db\_xref="teaxon:9913" /clone="9BOV2\_A09" /sex="Male" /notes"Organ: Abomasum; Vector: pAgen-1; Site 1: EcoRV; Site 2: NotI; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers. Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum" /tiasue\_type="Pooled" /dev\_stage="Multiple" /lab\_host="DH10B T1 phage resistant" /clone\_lib="BARC 9BOV" organism="Bos taurus" . .732 sequencing. GI:45064530 G. Baumann l Genomics <u>,</u> Beltsville, Score 35.2; Di Pred. No. 13; 0; Mismatches Lab ₫ DB 20705, USA and trimmed with phred 43; 7; 5 -minscore 12 Length Indels 190 USA 732; EST 04-MAR-2004 0 ; identified Gaps and 146 70 <u></u>

TITLE JOURNAL COMMENT VERSION KEYWORDS RESULT 14 DN526096 FEATURES DEFINITION 昂 8 昂 Ş REFERENCE SOURCE ORIGIN FEATURES Snoor ORGANISM AUTHORS Matches Query Match Best source Bource Local 
 11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAAATGGGCAAAC 70

		</td 659 71 61; Tel: Seq g High Seq cross\_match v0.990329. Plate: RLK8044 row: A Single pass sequencing. Bases called trimmed with the aid of the trim\_alt USDA, ARS, US Meat Animal PO Box 166, Clay Center, 1 Wray,J.E. and Keele,J.W. A second set of bovine ESTs Unpublished (2003) 1 (bases 1 to 825) Smith, T.P.L., Rober Bos taurus DN526096 825 bp mRNA linear 1270831 MARC 7BOV Bos taurus cDNA 5', mRNA sequence. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; DN526096.1 EST. DN526096 by cross\_match using options Plate: 2 row: D column: 12 Email: smith@email.marc.usda.gov rax: Contact: Smith TPL Pecora; Bovidae; Bos taurus (cow) 0.000925 using options -trim\_alt '' -trim\_fasta. Vector identified by cross\_match using options -minmatch 12 -minscore 12 Similarity AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 702 te: RLK8044 row: A column: 11
primer: GTAATACGACTCACTATAGGG. primer: CCTATTTAGGTGACACTATAGAAC 402 762 4366 402 762 4390 Conservative quality sequence stop: Location/Qualifiers /tissue\_type="Epithelial, Muscle"
/dev\_stage="Lactating, Neonatal"
/lab\_host="PHIOB TonA"
/clone\_lib="BARC 8BOV"
/nctes="Organ: Intestine; Vector: pCMVSport6.1; Site 1:
NorI; Site 2: BCoRI; Normalized cow cDNA intestinal
library in pCMVsport6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum" /organism="Bos taurus" /mol\_type="mRNA" /db\_xref="taxon:9913" ocation/Qualifiers "tissue\_type="pooled" /db\_xref="taxon:9913" /clone="8BOV\_2D12" /sex="Female" "strain="Holstein" 100 organism="Bos taurus" GI:60971328 .825 22.9%; Roberts, A.J., \_type="mRNA Bovinae; Bos. 0 ;; Score 35.2; DB 7; Pred. No. 13; 0; Mismatches 43; Bases called with phred v0.020425 the trim\_alt option. Vector ident: NB Research Center NB 68933-0166, USA Echternkamp,S.E., from pooled-tissue normalized libraries 742. H 43; Length 7.42; Indels Chitko-McKown,C.G., identified EST 11-MAR-2005 <u>,</u> Gaps 'n and with 658 0 Ś B ą DEFINITION ORIGIN FEATURES 昂 8 뭥 8 COMMENT REFERENCE ORGANISM KEYWORDS VERSION DN523404/c LOCUS RESULT 15 ORIGIN Matches Best Query Match TITLE AUTHORS Matches Best Query Match JOURNAL source Local Local 803 265 205 21 H 11 TECCTCTEAAGTCCACACTEAAACAAACTTCAECCTACTCATETCCCTAAAAATGEECAAAC 70 61; 61; Seq primer: cross match v0.990329. Plate: RLK8044 row: A column: 11 Seq primer: TAGAAGGCACAGTCGAGG. Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425. trimmed with the aid of the trim\_alt option. Vector identi Tel: 402 762 4366 Fax: 402 762 4390 USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, U Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keele,J.W. A second set of bovine ESTs from pooled-tissue normalized librari Unpublished (2003) Bos taurus 941 DD522404 94 D1266895 MARC 7BOV Bos taurus D523404 1 GI:60966258 D5523404 1 GI:60966258 EST Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; LauraBiatheria; Cetartiodactyla; Ruminantia; Bos taurus Pecora; Bovidae; Bovinae; Bos. Similarity Contact: Smith TPL Similarity TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAAC AATTTATTCAGAAGTGAAAAAAAAAGGAAGGAACCTGTCCTGCT 308 TGCCCAGGAATTAAAAAATAAAGCAACTTCAGCCTCCCCATCTCCAACAAATACAGAAAC (bases 1 to 941 Conservative Conservative /lab host="DH10B"
/clone\_lib="MARC 7BOV"
/clone="Wector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled From multiple tIssues
including ovary, hindbrain, uterus, and day-30 whole
embryos." /note="vector: pcDNA3.1; Site\_1: EcoRI; Site\_2: No Library made with RNA pooled From multiple tissues including ovary, hindbrain, uterus, and day-30 who embryos." embryos. /lab\_host="DH10B" /clone\_lib="MARC ' /mol\_type="mRNA" /db\_xref="taxon:9913" organism="Bos taurus" 'tissue\_type="pooled" ocation/Qualifiers (cow) .941 22.9%; 22.9%; 58.7%; \_lib="MARC 7BOV" , ;; Score 35.2; D Pred. No. 14; O; Mismatches 0; Score 35.2; Pred. No. 14; Mismatches bp mRNA linear cDNA 3', mRNA sequence. DB 멂 8; 43; 43; 8 ; USA Length 941; Length 825; Indels Indels normalized libraries identified . 0; EST 11-MAR-2005 <u>,</u> 2: NotI; whole Gaps Gaps ò and with 744 70 264 <u>,</u> <u>,</u>

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Mon Apr 24 07:43:11 2006 ₿ Search completed: April 18, 2006, 15:20:35 Job time : 751.823 веся ! 743 AATTTATTCAGAAGTGAAAAAACAGTAAAGGAACCTGTCCTGCT 700 us-09-884-901a-8.rst

c 14 32.2 c 15 31.6 c 17 31.4 19 31.2 c 20 31.2 c 21 31.2 c 22 31.2 c 23 31.2 31.2 c 23 31.2 c 31.2						Pred. No score gro and is de	Database :	Post-processing:	Minimum DB seq Maximum DB seq	Total number o	Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:	OM nucleic - n	
20.9     645     4     US-09-225-065A-103589       20.6     662     4     US-09-925-065A-103589       20.5     31134     8     US-10-741-600-18001       20.4     88191     3     US-09-799-799-3       20.3     257     3     US-09-864-761-25083       20.3     567     3     US-09-864-761-25083       20.3     561     3     US-09-864-761-25083       20.3     511     4     US-09-925-065A-370446       20.3     611     4     US-09-925-065A-370446       20.3     611     4     US-09-925-065A-370448       20.3     611     4     US-09-925-065A-370448       20.1     939     8     US-10-774-355A-177	98.1         154         6         US-10-100-235-11         Sequence           23.6         568         9         US-10-972-079-50807         Sequence           23.6         574         9         US-10-972-079-50806         Sequence           21.2         645         4         US-09-925-065A-103590         Sequence	100.0         10527         6         US-10-287-964-95         Sequence           100.0         16963         7         US-10-741-601-5756         Sequence           100.0         16963         8         US-10-741-600-17945         Sequence           100.0         16963         8         US-10-741-600-17945         Sequence           100.0         16963         8         US-10-741-600-17945         Sequence           100.0         41907         3         US-09-967-013-5         Sequence	100.0         328         3         US-09-864-901-9         Sequence           100.0         328         3         US-09-864-901-9         Sequence           100.0         771         3         US-09-864-901-4         Sequence           100.0         10527         3         US-09-863-733A-100         Sequence           100.0         10527         5         US-10-116-420-100         Sequence	Query Match Length DB ID Description		No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.	<pre>Published Applications_NA_Main:* 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:* 3: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:* 3: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:* 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:* 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:* 7: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:* 8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:* 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:* 10: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*</pre>	g: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	length: 0 length: 2000000000	f hits satisfying chosen parameters: 19587084	9793542 ведв, 4134689005 residues	IDENTITY NUC Gapop 10.0 , Gapext 1.0	US-09-884-901A-8 154 1 gtttgtgtgctgcctctgaaggtcagagacctctctgggc 154	April 18, 2006, 12:46:08 ; Search time 153.338 Seconds (without alignments) 8305.080 Million cell updates/sec	nucleic search, using sw model	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
RESULT 2 US-09-884-901-9 ; Sequence 9, Application US/09884901 ; Patent No. US20020076796A1 ; GINERAL INFORMATION: ; APPLICANT: Miao, Carol ; APPLICANT: Miao, Carol ; APPLICANT: Max, Mark ; TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use	Db 121 GAAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154	QY         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACACA	1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCC 	Query Match 100.0%; Score 154; DB 3; Length 154; Best Local Similarity 100.0%; Pred. No. 2e-43; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	; TIPS: UNA ; OGANISH: HOMOSapien US-09-884-901-8	SOFTWARE: PatentIn version 3.0 SEQ ID NO 8 LENGTH: 154		RESULT 1 US-09-884-901-8		30 19.5 1931 6 US-10-027-632-259734 30 19.5 1931 6 US-10-027-632-259735	42 30 19.5 1931 5 US-10-027-632-259734 43 30 19.5 1931 5 US-10-027-632-259735	30 19.5 475 6 US-10-027-632-43555 30 19.5 657 10 US-11-097-143-39248 30 19.5 658 5 US-10-255-536-144	35 30.2 19.6 552 6 US-10-029-366-8280 36 30.2 19.6 646 8 US-10-767-755-5679 37 30.2 19.6 113819 8 US-10-719-993-6852 38 30 19.5 475 5 US-10-027-632-43555	30.4 19.7 613 4 US-09-925-065A-757427 30.4 19.7 1400 7 US-10-322-281-643 30.4 19.7 2292 7 US-10-437-963-43156 30.4 19.7 29340 7 US-10-322-281-642	30.6 19.9 20993 0 US-10-VUY-112-13 30.6 19.9 26993 7 US-10-394-948-7 30.6 19.9 145597 7 US-10-624-149A-2	22554

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RESULT 4 US-09-863-733A-100 ; Sequence 100, Application US/09863733A ; Publication No. US20030082537A1 ; GENERAL INFORMATION:	<pre>US-09-864-901-4 iS-genence 4, Application US/09884901 iFacent No. US202007679801 iSequence 4, Application US/09884901 iSequence 4, Application US/09884901 iSequence 4, Application US/09884901 iSequence 1, Application US/09884,901 iSequence 1, Application US/09884,901 iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use iTTLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use inventse interval invention 3.0 iSoftwake: PatentIn version 3.0 iSoftwake: PatentIn version 3.0 iSoftwake: PatentIn version 3.0 iSoftwake: Local Similarity 100.0%; Score 154; DB 3; Length 771; Best Local Similarity 100.0%; Score 154; DB 3; Length 771; Hatches 154; Conservative 0, Mismatches 0; Indels 0; Gaps 0; iB articlearcerectoreconcertereconcert</pre>	<pre>FILE REFERENCE: UDFW-1-17396 CURRENT APPLICATION NUMBER: US/09/884,901 CURRENT APPLICATION NUMBER: US/09/884,901 PHIOR FILING DATE: 2000-06-20 NUMBER OF SEQ ID NOS: 18 FORGALE: Patentin version 3.0 SEQ ID NO 9 LEARTH: 328 TYPE: DNA CORGANISM: Homo Sapien US-09-884-901-9 Cuery Match Best Local Similarity 100.0%; Score 154; DB 3; Length 328; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0; SC IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII</pre>
Query Match 100.0%; Score 154; DB 5; Length 10527; Best Local Similarity 100.0%; Pred. No. 7e-43; Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACTTCAGCCTACTCATGTCCCCTAAA 60	bb       9728       Aldodrindchardschardenewskindenenewskindenewskindenewskindenewskindenenewsk	APPLICANT: Stanton, Jr., Vincent P. TITLE OF INVENTION: METHODS FOR GENETIC ANALYSIS OF DNA FILE REFERENCE: 11926-113001 CURRENT PELLATION NUMBER: 09/697,028 PRIOR APPLICATION NUMBER: 09/697,028 PRIOR APPLICATION NUMBER: 09/697,028 PRIOR APPLICATION NUMBER: 09/697,013 PRIOR APPLICATION NUMBER: 0000-10-25 PRIOR APPLICATION PRIOR PRICECATION NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 0000-10-25 PRIOR APPLICATION PRICE NUMBER: 00000-10-25 PRIOR APPLICATION PRICE NUMBER: 00000-10-25 PRIOR APPLICATION PRICE NUMBER: 000000-10-25 PRIOR APPLICATION NUMBER: 000000000000000000000000000000000000

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RESULT 7 US-10-741-601-5756 Sequence 5756, Application US/10741601 Publication No. US20040166519A1 GENERAL INFORMATION: Michele et al. APPLICANT: CARGILL, Michele et al. TITLE OF INVERTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVERTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVERTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CURRENT APPLICATION UNMER: US/10/741,601 CURRENT APPLICATION NUMBER: US/10/741,601 CURRENT FILLING DATE: 2003-12-22 SOFTWARE: PABLEEQ for Windows Version 4.0 SEQ ID NO 5756 LENGTH: 16963 TYPE: DNA CURANISM: Homo sapiens	Query Match       100.0%; Score 154; DB 6; Length 10527;         Best Local Similarity 100.0%; Pred. No. 7e-43;       Indels 0; Gaps 0;         Qy       1 GTTTGTGTGCTGCCTCTGAAGTCCACACTEAACAAACTTCAGGCTACTCATGTCCCTAAA 60         Db       9668 GTTTGTGTGCTGCTCTGAAGTCCACACTEAACAAACTTCAGGCTACTCATGTCCCTAAA 9727         Qy       61 ATGGGCAAACATTGCAAGTCCACACCTEAACAAACATCAGGCCTGCCTGCCTGACCTT 120         Db       9728 ATGGGCAAACATTGCAAGCAGCAGCAACAGCAAACAACACAGGCCTCCCTGCCTG	PESCUT? 6 US-10-287-964-95 ; Sequence 95, Application US/10287964 publication No. US20030219769A1 ; GENERAL INFORMATION: APPLICANT: Dilon, Jeffrey APPLICANT: Zillmann, Martin APPLICANT: Stanton, Jr., Vincent P. APPLICANT: Stanton, Jr., Vincent P. APPLICANT: Stanton, Jr., Vincent P. TITLE OF INVENTION: POLYMORPHIC SITES FILE REFERENCE: 11926-016002 CURRENT APPLICATION NUMBER: US/10/287,964 CURRENT FILING DATE: 2000-10-25 PRIOR APPLICATION NUMBER: US 00/566,998 PRIOR APPLICATION NUMBER: US 00/206,613 PRIOR FILING DATE: 2000-05-23 NUMBER OF SEQ ID NOS: 95 SEQ ID NOS 95	Db       9668       GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAACTTCAGCCTACTCATGTCCCCTAAA         QY       61       ATGGGCAAACATTGCAAGCCACACAGCAAACAACAACACAGCCTACTCATGTCCCCTGACCTT       120         Db       9728       ATGGGCAAACATTGCAAGCAGCAAACAGCAAACAAACAACAGCCTCCCTGCCTG
RESULT 9 US-09-967-013-5 Sequence 5, Application: US/09967013 Patent No. US20020045840A1 GENERAL INFORMATION: ALL VINCENT P. TITLE OF INVENTION: METHOD FOR GENETIC ANALYSIS OF APOE DNA TITLE OF INVENTION: METHOD FOR GENETIC ANALYSIS OF APOE DNA TITLE OF INVENTION: METHOD FOR GENETIC ANALYSIS OF APOE DNA TITLE OF INVENTION: MAD USES THEREOF FILE REFERENCE: 11926-022001 CURRENT APPLICATION NUMBER: US/09/967,013 CURRENT APPLICATION NUMBER: 05/206,613 PRIOR APPLICATION NUMBER: 2000-05-23 NUMBER OF SEQ ID NOS: 91 SEQ ID NO 5 SEQ ID NO 5 LENGTH: 41907 TYPE: DNA ORGANISM: Homo sapiens US-09-967-013-5	Matches       154;       Conservative       0;       Mismatches       0;       Indels       0;       Gaps       0;         QY       1       GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGGCTACTCATGTCCCTAAA       60	9       1000000000000000000000000000000000000	Query Mat Best Loca Matches 159 160

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<pre>Mission () (us-10-972-079-50807/c Sequence 50807, Application US/10972079 Publication No. US20050153317A1 GENERAL INFORMATION: APPLICANT: NOI GENOMICS, INC. APPLICANT: DENISE, Sue K. APPLICANT: DENISE, Sue K. APPLICANT: DENISE, Sue K. APPLICANT: DENISE, Sue K. APPLICANT: BATES, Stephen APPLICANT: BATES, Stephen TITLE OF INVENTION: METHODS &amp; SYSTEMS FOR INFERRING TRAITS TO BREED &amp; MANAGE NON-BEEF TITLE OF INVENTION: LIVESTOCK FILE REFERENCE: MMIIII0-2</pre>		Query Match       98.1%; Score 151; DB 6; Length 154;         Best Local Similarity.       100.0%; Pred. No. 2.2e-42;         Matches       151; Conservative       0; Mismatches       0; Indels       0; Gaps       0;         Qy       1 GTTTGTGTGCCTCCTGAAGTCCAACTTGAACTTCAACCTTCATCTATCT	NVENTION: F NVENTION: F ENCE: 0800 PLICATION N PLICATION DATB: LING DATB: 20 ICATION NG SEQ ID NOS: SEQ  SULT 10 -10-100-235-11 Sequence 11, Application US/10100235 Publication No. US20030147853A1 PELICANT: MCCLELLAND, Alan APPLICANT: SCOLLAY, Roland	Query Match       100.0%;       Score 154;       DB 3;       Length 41907;         Best Local Similarity       100.0%;       Pred. No. 1.1e-42;         Matches 154;       Conservative       0;       Mismatches       0;       Indels       0;         Qy       1       GTTTGTGTGCGCGCCTCTGAAGTCCACACTGAACATGCACACTGATGTCCATGTCCCTAAA       60       []]	
Qy       0       Antification and antification and Mapping of Single         Bb       411 GCACTCTGCCAGCAGCGCATCTCGCATGCAGGCACCACCCTCCCT	Query Ma Best Loc Matches	PRIOR FILING DATE: 2003-10-24 NUMBER OF SEQ ID NOS: 96631 SOFTWARE: PatenTIN version 3.1 SEQ ID NO 50806 LENGTH: 574 TYPE: DNA ORGANISM: Chicken 19866894298036_4	RESULT 12 US-10-972-079-50806/c Sequence 50806, Application US/10972079 Publication No. US20050153317A1 GENERAL INFORMATION: APPLICANT: MMI GENOMICS, INC. APPLICANT: DENISE, SUE K. APPLICANT: DENISE, SUE K. APPLICANT: MAINER, Richard APPLICANT: HOLSE, Stephen APPLICANT: HOLM, Tom TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BBE TITLE OF INVENTION: LIVESTOCK FILE REFERENCE: MMI1110-2 CURRENT APPLICATION NUMBER: US/10/972,079 CURRENT PILING DATE: 2004-10-22 FROM APPLICATION NUMBER: US/0514,333	Qy       7 GEGCTGCCTCTGAAGTCCACACTGAACAACTTCAGCCTACTANTGTGGC 66         Db       465 GEGCTGCCATTACAGCCGGCGGCGGCGAGCATCCGCGGCAGCGTCGCCTAGCAATGGCC 406         Qy       67 AAACATTGCCAAGCAGCAACAGCCAACCACCGCGGCAGCCTCGCCTGGCCTAGCAATGGCC 406         Qb       405 GCACTCTGCCAAGCAACCAACGAGCAACACACACCCTCCCT	<pre>; CURRENT APPLICATION NUMBER: US/10/972,079 ; CURRENT FILING DATE: 2004-10-22 ; PRIOR APPLICATION NUMBER: US 60/514,333 ; PRIOR FILING DATE: 2003-10-24 ; NUMBER OF SEQ ID NOS: 96631 ; SOPTWARE: PatentIN version 3.1 ; SOPTWARE: PatentIN version 3.1 ; SEQ ID NO 50807 ; LENGTH: 568 ; TYPE: DNA ; ORGANISM: Chicken 19866894298036_5 US-10-972-079-50807 Ouery Match 23.6%; Score 36.4; DB 9; Length 568; Best Local Similarity 56.0%; Fred. No. 0.037; Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;</pre>

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OY       117 CCTTGGAGGCTGGGGCAGAGGTCAGAGACCTCTCTG       151         Db       125 GCCTTGTAGAGGTAAAAGAGGTCATATTTTATTCTG       159	QY 57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAAACAGCACAGGCCTGCCT	Query Match 20.9%; Score 32.2; DB 4; Length 645; Best Local Similarity 57.9%; Pred. No. 1.1; Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;	; SOFTWARKE: FASTSEQ FOF WINDOWS VEESION 4.0 ; SEQ ID NO 103589 ; LENGTH: 645 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-925-065A-103589	PRIOR FILING DATE: 2001-01-16 PRIOR APELICATION NUMBER: US 60/289,846 PRIOR FILING DATE: 2001-05-09 NUMBER OF SEO ID NOS: 957086 NUMBER OF SEO ID NOS: 957086	0/250, 0/250,	CURRENT APPLICATION NUMBER: US/09/9 CURRENT FILING DATE: 2001-08-08 PRIOR APPLICATION NUMBER: US 60/243 PRIOR FILING DATE: 2000-10-24 PRIOR FILING DATE: 2000-10-24	GENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135	RESULT 14 US-09-925-065A-103589 ; Sequence 103589, Application US/09925065A ; publication No. US20050228172A9	OY 117 CCTTGGAGCTGGGGGAGAGGGTCAGAGACCTCTCTG 151 	Oy         57         Taaaatgeggaaacattgcaagcaagcaagcaaacacacacacacccccccc	Query Match 21.2%; Score 32.6; DB 4; Length 645; Best Local Similarity 58.9%; Pred. No. 0.81; Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;	CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 PRIOR FILING DATE: 2000-10-24 PRIOR FILING DATE: 2000-10-24 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-11-20 PRIOR FILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 SOPTWARE: PASSEC ID NOS: 957086 SOPTWARE: FASSEC for Windows Version 4.0 LENGTH: 645 FYEE: DNA ORGANISM: Homo Sapiens
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PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-10-24 PRIOR RILLING DATE: 2000-11-20 PRIOR RILLING DATE: 2000-11-20 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR RILLING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 957086 SOPTWARE: PRAESEQ for Windows Version 4.0 IENGTH: 662 IENGTH: 662 VIGGANISM: Homo sapiens US-09-925-065A-782496 Search completed: April 18, 2006, 13:17:10 Job time : 155.338 secs 昂 2 RESULT 15 US-09-925-065A-782496/c 昂 Ś 昂 Ş Sequence 782436, Application US/09925065A Publication No. US20050228172A9 SENERAL INFORMATION: Application and Mapping of Single TITLE OF INVENTION: Identification and Mapping of Single TITLE REFERENCE: 108827.135 CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 Query Match 20.6%; Score 31.8; D) Best Local Similarity 51.8%; Pred. No. 1.6; Matches 72; Conservative 0; Mismatches 131 CAGAGGTCAGAGACCTCTC 149 81 AAAAGAAAAAGAAAAATAGCAGACTCATATCTGTGCCTTCCCCTGGATCTGGGACGTGGCC 22 11 TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCGAAAC 70 21 AGAGAGAGGGÁGCCCTCCC 3 DB 4; Length 662; 67; Indels 0; Сарв

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Maccines 1 1 87845 61 87905 121 121 87965 SULT 2 -10-995-561 Sequence 13	SM: Hon 086-27 tch al_Simi	 Зно	ESULT 1 S-11-121-086-27 S-11-121-086-27 Publication No. US20050 ERNERAL INFORMATION: APPLICANT: NULSEN, TI APPLICANT: NULSEN, TI PILE REFERENCE: 09138 CURRENT APPLICATION NUME FILE REFERENCE: 00138 CURRENT APPLICATION NUME PRIOR APPLICATION NUME PRIOR PILING DATE: 200 NUMBER OF SEO ID NOS:		42 29.2 19.0 43 29.2 19.0 44 29.2 19.0 44 29.2 19.0 45 29.2 19.0 45 29.2 19.0	39 29.6 19.2 40 29.6 19.2 41 39 3 19.0	37 29.6 19.2 38 29.6 19.2	29.8 19.4 29.6 19.2 29.6 19.2	30         30         19.5           31         29.8         19.4           32         29.8         19.4           33         29.8         19.4	26 30.2 19.6 27 30 19.5 28 30 19.5 29 30 19.5	30.4 19.7 30.4 19.7 30.2 19.6	19       31.2       20.3         20       31.2       20.3         21       31.2       20.3         22       31.2       20.3
Maccines 1 1 87845 61 87905 121 121 87965 SULT 2 -10-995-561 Sequence 13	SM: Hon 086-27 tch al_Simi	 Зно	ESULT 1 S-11-121-086-27 Sequence 27, Application US/1 Publication No. US20050266455 GENERAL INFORMATION: TIM S. APPLICANT: NULSEN, KIRSTER TITLE OF INVENTION: NUCLEIC FILE REFERENCE: 09138.6000- CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 2004-05-0 PRIOR FILING DATE: 2004-05-0 NUMBER OF SEO ID NOS: 107		42 29.2 19.0 499 43 29.2 19.0 499 44 29.2 19.0 507 44 29.2 19.0 507 45 29.2 19.0 507	39 29.6 19.2 726 40 29.6 19.2 3885 41 39.3 19.0 200	37 29.6 19.2 571 38 29.6 19.2 726	29.8 19.4 1415 29.6 19.2 567 29.6 19.2 567	30         30         19.5         1931           31         29.8         19.4         1204           32         29.8         19.4         1204           33         29.8         19.4         1400	26 30.2 19.6 1457619 27 30 19.5 1931 28 30 19.5 1931 29 30 19.5 1931 29 30 19.5 1931	30.4 19.7 613 30.4 19.7 169495 30.2 19.6 996	19       31.2       20.3       627         20       31.2       20.3       627         21       31.2       20.3       627         22       31.2       20.3       627
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Maccines 1 1 87845 61 87905 121 121 87965 SULT 2 -10-995-561 Sequence 13	SM: Homo Bapiens 086-27 tch 100.0%; al Similarity 100.0%;	 Зно	RESULT 1 US-11-121-086-27 Sequence 27, Application US/11121086 Publication No. US20050366459A1 GENERAL INFORMATION: APPLICANT: NUCLEEN, TIM S. APPLICANT: NUCLENC, KIRSTEN V. TITLE OF INVENTION: NUCLEIC ACID PROBES FILE REFERENCE: 09138.6000-00000 CURRENT APPLICATION NUMBER: US/11/121,0 FILE REFERENCE: 09138.60/507.570 PRIOR APPLICATION NUMBER: 60/567,570 PRIOR FILING DATE: 2004-05-04 . NUMMER OF SEO ID NOS: 107		42 29.2 19.0 499 43 29.2 19.0 499 44 29.2 19.0 507 44 29.2 19.0 507 45 29.2 19.0 507	39 29.6 19.2 726 40 29.6 19.2 3885 41 39.3 19.0 200	37 29.6 19.2 571 38 29.6 19.2 726	29.8 19.4 1415 29.6 19.2 567 29.6 19.2 567	30         30         19.5         1931           31         29.8         19.4         1204           32         29.8         19.4         1204           33         29.8         19.4         1400	26 30.2 19.6 1457619 27 30 19.5 1931 28 30 19.5 1931 29 30 19.5 1931 29 30 19.5 1931	30.4 19.7 613 30.4 19.7 169495 30.2 19.6 996	19       31.2       20.3       627       10         20       31.2       20.3       627       10         21       31.2       20.3       627       10         22       31.2       20.3       627       10
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Maccines 1 1 87845 61 87905 121 121 87965 SULT 2 -10-995-561 Sequence 13	SM: Homo sapiens 086-27 tch 100.0\$; al Similarity 100.0\$;		21,08		42 29.2 19.0 499 43 29.2 19.0 499 44 29.2 19.0 507 44 29.2 19.0 507 45 29.2 19.0 507	39 29.6 19.2 726 40 29.6 19.2 3885 41 39.3 19.0 200	37 29.6 19.2 571 38 29.6 19.2 726	29.8 19.4 1415 29.6 19.2 567 29.6 19.2 567	30         30         19.5         1931           31         29.8         19.4         1204           32         29.8         19.4         1204           33         29.8         19.4         1400	26 30.2 19.6 1457619 27 30 19.5 1931 28 30 19.5 1931 29 30 19.5 1931 29 30 19.5 1931	30.4 19.7 613 30.4 19.7 169495 30.2 19.6 996	19       31.2       20.3       627       10       US-10-301-480         20       31.2       20.3       627       10       US-10-301-480         21       31.2       20.3       627       10       US-10-301-480         22       31.2       20.3       627       10       US-10-301-480         22       31.2       20.3       627       10       US-10-301-480
Maccines 1 1 87845 61 87905 121 121 87965 SULT 2 -10-995-561 Sequence 13	SM: Homo sapiens 086-27 tch 100.0%; Score 154; DB 14; al Similarity 100.0%; Pred. No. 3.3e-39;		DBES AND NUCLEIC 21,086		1         2         2         1         0         499         6         US-109-925-065A-367162           43         29.2         19.0         499         6         US-09-925-065A-367163           43         29.2         19.0         499         6         US-109-925-065A-367163           44         29.2         19.0         507         10         US-10-301-480-437513           45         29.2         19.0         507         10         US-10-301-480-437514	39 29.6 19.2 726 B US-10-750-623-56490 40 29.6 19.2 3885 11 US-11-079-463-930 41 29.7 19.7 200 14 US-11-098-686-6769	37 29.6 19.2 571 6 US-09-925-065A-143037 38 29.6 19.2 726 8 US-10-750-185-50490	29.8 19.4 1415 14 US-11-136-527-2133 29.6 19.2 567 10 US-10-301-480-237751 29.6 19.2 567 10 US-10-301-480-851160	30 19.5 1931 10 US-10-301-480-707952 31 29.8 19.4 1204 8 US-10-750-185-39545 32 29.8 19.4 1204 8 US-10-750-623-39545 33 29.8 19.4 1400 14 US-11-136-527-6229	26         30.2         19.6         14.57619         14         US-11-098-686-8739           27         30         19.5         1931         9         US-10-301-480-94542           28         30         19.5         1931         9         US-10-301-480-94543           29         30         19.5         1931         10         US-10-301-480-94543	30.4 19.7 69495 14 US-11-121-086-61 30.4 19.7 169495 14 US-11-121-086-61 30.2 19.6 996 14 US-11-098-686-9756	19       31.2       20.3       627       10       US-10-301-480-440499         20       31.2       20.3       627       10       US-10-301-480-1053906         21       31.2       20.3       627       10       US-10-301-480-1053907         21       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053908
Maccines 1 1 87845 61 87905 121 121 87965 SULT 2 -10-995-561 Sequence 13	SM: Homo sapiens 086-27 tch 100.0%; Score 154; DB 14; Length al Similarity 100.0%; Pred. No. 3.3e-39;		DBES AND NUCLEIC 21,086		1         2         2         1         0         499         6         US-109-925-065A-367162           43         29.2         19.0         499         6         US-09-925-065A-367163           43         29.2         19.0         499         6         US-109-925-065A-367163           44         29.2         19.0         507         10         US-10-301-480-437513           45         29.2         19.0         507         10         US-10-301-480-437514	39 29.6 19.2 726 B US-10-750-623-56490 40 29.6 19.2 3885 11 US-11-079-463-930 41 29.7 19.7 200 14 US-11-098-686-6769	37 29.6 19.2 571 6 US-09-925-065A-143037 38 29.6 19.2 726 8 US-10-750-185-50490	29.8 19.4 1415 14 US-11-136-527-2133 29.6 19.2 567 10 US-10-301-480-237751 29.6 19.2 567 10 US-10-301-480-851160	30 19.5 1931 10 US-10-301-480-707952 31 29.8 19.4 1204 8 US-10-750-185-39545 32 29.8 19.4 1204 8 US-10-750-623-39545 33 29.8 19.4 1400 14 US-11-136-527-6229	26         30.2         19.6         14.57619         14         US-11-098-686-8739           27         30         19.5         1931         9         US-10-301-480-94542           28         30         19.5         1931         9         US-10-301-480-94543           29         30         19.5         1931         10         US-10-301-480-94543	30.4 19.7 69495 14 US-11-121-086-61 30.4 19.7 169495 14 US-11-121-086-61 30.2 19.6 996 14 US-11-098-686-9756	19       31.2       20.3       627       10       US-10-301-480-440499         20       31.2       20.3       627       10       US-10-301-480-1053906         21       31.2       20.3       627       10       US-10-301-480-1053907         21       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053908
Maccines 1 1 87845 61 87905 121 121 87965 SULT 2 -10-995-561 Sequence 13	SM: Homo sapiens 086-27 tch 100.0%; Score 154; DB 14; Length 153142; al Similarity 100.0%; Pred. No. 3.3e-39;		DBES AND NUCLEIC 21,086		1         2         2         1         0         499         6         US-109-925-065A-367162           43         29.2         19.0         499         6         US-09-925-065A-367163           43         29.2         19.0         499         6         US-109-925-065A-367163           44         29.2         19.0         507         10         US-10-301-480-437513           45         29.2         19.0         507         10         US-10-301-480-437514	39 29.6 19.2 726 B US-10-750-623-56490 40 29.6 19.2 3885 11 US-11-079-463-930 41 29.7 19.7 200 14 US-11-098-686-6769	37 29.6 19.2 571 6 US-09-925-065A-143037 38 29.6 19.2 726 8 US-10-750-185-50490	29.8 19.4 1415 14 US-11-136-527-2133 29.6 19.2 567 10 US-10-301-480-237751 29.6 19.2 567 10 US-10-301-480-851160	30 19.5 1931 10 US-10-301-480-707952 31 29.8 19.4 1204 8 US-10-750-185-39545 32 29.8 19.4 1204 8 US-10-750-623-39545 33 29.8 19.4 1400 14 US-11-136-527-6229	26         30.2         19.6         14.57619         14         US-11-098-686-8739           27         30         19.5         1931         9         US-10-301-480-94542           28         30         19.5         1931         9         US-10-301-480-94543           29         30         19.5         1931         10         US-10-301-480-94543	30.4 19.7 69495 14 US-11-121-086-61 30.4 19.7 169495 14 US-11-121-086-61 30.2 19.6 996 14 US-11-098-686-9756	19       31.2       20.3       627       10       US-10-301-480-440499         20       31.2       20.3       627       10       US-10-301-480-1053906         21       31.2       20.3       627       10       US-10-301-480-1053907         21       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053908
1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAACTTCAGCCTACTCATGTCCCTAAA         1 GTTTGTGTGTGCTGCCTCTGAAGTCCACACACAACTTCAGCCTACTCATGTCCCTAAA         87845 GTTTGTGTGCTGCCCTCTGAAGTCCACACACACAACTTCAGCCTACTCATGTCCCTGACCA         61 ATGGGCAAACATTGCAAGCAGCAAACAGCAAACACACACA	SM: Homo sapiens 086-27 tch 100.0%; Score 154; DB 14; Length 153142; al Similarity 100.0%; Pred. No. 3.3e-39;		21,08		1         2         2         1         0         499         6         US-109-925-065A-367162           43         29.2         19.0         499         6         US-09-925-065A-367163           43         29.2         19.0         499         6         US-109-925-065A-367163           44         29.2         19.0         507         10         US-10-301-480-437513           45         29.2         19.0         507         10         US-10-301-480-437514	39 29.6 19.2 726 B US-10-750-623-56490 40 29.6 19.2 3885 11 US-11-079-463-930 41 29.7 19.7 200 14 US-11-098-686-6769	37 29.6 19.2 571 6 US-09-925-065A-143037 38 29.6 19.2 726 8 US-10-750-185-50490	29.8 19.4 1415 14 US-11-136-527-2133 29.6 19.2 567 10 US-10-301-480-237751 29.6 19.2 567 10 US-10-301-480-851160	30 19.5 1931 10 US-10-301-480-707952 31 29.8 19.4 1204 8 US-10-750-185-39545 32 29.8 19.4 1204 8 US-10-750-623-39545 33 29.8 19.4 1400 14 US-11-136-527-6229	26         30.2         19.6         14.57619         14         US-11-098-686-8739           27         30         19.5         1931         9         US-10-301-480-94542           28         30         19.5         1931         9         US-10-301-480-94543           29         30         19.5         1931         10         US-10-301-480-94543	30.4 19.7 69495 14 US-11-121-086-61 30.4 19.7 169495 14 US-11-121-086-61 30.2 19.6 996 14 US-11-098-686-9756	19       31.2       20.3       627       10       US-10-301-480-440499         20       31.2       20.3       627       10       US-10-301-480-1053906         21       31.2       20.3       627       10       US-10-301-480-1053907         21       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053907         22       31.2       20.3       627       10       US-10-301-480-1053908
1 GTTTGTGTGCTGCTGCTGCAGACAAACTTCAGCCTACTCATGTCCCTAAA 60         1 GTTTGTGTGCTGCCTGCTGAAGTCCACACTGAAAACTTCAGCCTACTCATGTCCCTAAA 60         87845 GTTTGTGTGCTGCCTCCTGAAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 60         61 ATGGGCAAACATTGCAAGCACACCTGAACAAACACACACGCCTCCCTGCCTG	SM: Homo sapiens 086-27 tch 100.0%; Score 154; DB 14; Length 153142; al Similarity 100.0%; Pred. No. 3.3e-39;		DBES AND NUCLEIC 21,086		1         2         2         1         0         499         6         US-109-925-065A-367162           43         29.2         19.0         499         6         US-09-925-065A-367163           43         29.2         19.0         499         6         US-109-925-065A-367163           44         29.2         19.0         507         10         US-10-301-480-437513           45         29.2         19.0         507         10         US-10-301-480-437514	39 29.6 19.2 726 B US-10-750-623-56490 40 29.6 19.2 3885 11 US-11-079-463-930 41 29.7 19.7 200 14 US-11-098-686-6769	37 29.6 19.2 571 6 US-09-925-065A-143037 38 29.6 19.2 726 8 US-10-750-185-50490	29.8 19.4 1415 14 US-11-136-527-2133 29.6 19.2 567 10 US-10-301-480-237751 29.6 19.2 567 10 US-10-301-480-851160	30 19.5 1931 10 US-10-301-480-707952 31 29.8 19.4 1204 8 US-10-750-185-39545 32 29.8 19.4 1204 8 US-10-750-623-39545 33 29.8 19.4 1400 14 US-11-136-527-6229	26         30.2         19.6         14.57619         14         US-11-098-686-8739           27         30         19.5         1931         9         US-10-301-480-94542           28         30         19.5         1931         9         US-10-301-480-94543           29         30         19.5         1931         10         US-10-301-480-94543	30.4 19.7 69495 14 US-11-121-086-61 30.4 19.7 169495 14 US-11-121-086-61 30.2 19.6 996 14 US-11-098-686-9756	19       31.2       20.3       627       10       US-10-301-480         20       31.2       20.3       627       10       US-10-301-480         21       31.2       20.3       627       10       US-10-301-480         22       31.2       20.3       627       10       US-10-301-480         22       31.2       20.3       627       10       US-10-301-480

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Title: Perfect score: Sequence:

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<pre>Publication No. US200007709441 Publication No. US20007709441 Publication No. US20007709441 Publication No. US20007709441 Publication Number Publication Number Publication Publication Publication No. US20007709441 Publication Number Publication Publication Publication Publication Number Publication Publication Publication Publication Publication Number Publication Publica</pre>	<pre>Publication No. US20050272054A1 SEPERAL INFORMATION: APPLICANT: CARDIVACULAR DISORDERS ASSOCIATED WITH ITITLE OF INVENTION: CARDIVACULAR DISORDERS AND DRUG RESPONSE, METHODS OF ITITLE OF INVENTION: DEFECTION AND USES THEREOF ITITLE OF INVENTION: DEFECTION AND USES THEREOF ITITLE OF INVENTION: DEFECTION AND USES THEREOF ICURARENT APPLICATION WHERE: US/10/995.561 CURARENT PILLING DATE: 2004-11-24 NUMBER OF SEC ID NOS: 65702 SEC ID NO: 1467 ICURARENT FRILING DATE: 2004-11-24 NUMBER OF SEC ID NOS: 65702 SEC ID NO: 1467 ICURARENT FILING DATE: 2004-11-24 NUMBER OF SEC ID NOS: 65702 SEC ID NO: 1467 ICURARENT FRIEND ID NO: 75 SCOTE 154. DB 8; Length 16963; Best Local Similarity 90.4%; Dreed No. 2.1e-39; Matches 153; CONSErvative 1; Mismatches 0; Indels 0; Gaps 0; Natches 153; CONSErvative 1; Mismatches 0; Indels 0; Gaps 0; ISO I STRUTTORICIFICTERIAGTICCACACTGAACAAACTAACAACAACAACAACAACAACAACAACAACAA</pre>
SULT 5 SULT 5 Sequence 840 Publication AENERAL ING TITLE OF II TITLE OF II TITLE OF II TITLE OF II TITLE OF II TITLE OF II CURRENT API CURRENT FII NUMBENT FII NUMBENT FII ORGANISM: -10-995-561 ORGANISM: -10-995-561 Set Local s Best Local s Atches 146 155 55 61 115	RESULT 4 US-10-995-561-75740 i Sequence 75740, Application US/10995561 Publication No. US20050772054A1 I SERVENTION: CARGILL, Michele et al. I SERVENTION: CREATIC POLYMORPHISMS ASSOCIATED WITH I TITLE OF INVENTION: CREATIC POLYMORPHISMS ASSOCIATED NEW RESPONSE, METHODS OF I TITLE OF INVENTION: CREATIC POLYMORPHISMS ASSOCIATED NEW RESPONSE, METHODS OF I CURRENT FILLING DATE: 2004-11-24 NUMBER OF SEQ ID NOS: 85702 SOFTWARE: FRACESO FOR MINDOWS VETSION 4.0 I SEQ ID NO 75740 QUERY MAECH Best Local Similarity 95.2%; Score 146.5; DB 8; Length 201; Best Local Similarity 95.3%; Fred. NO. 8, TITLES 0; Gaps 0; Matches 146; CONSERVATIVE 1; Mismatches 0; Indels 0; Gaps 0; Matches 146; CONSERVATIVE 1; Mismatches 0; Indels 0; Gaps 0; Matches 146; CONSERVATIVECARCHARCHARACHARACHARACHARACHARCHARCHARC

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pplication US 20060057564A1 N: Identifict N: In the Hu 08827.137 DN WUMBER: US 1 NUMBER: US 1 : 2002-08-09 NUMBER: US 1 : 2001-08-09 NUMBER: US 1 : 2001-08-00 NUMBER: US 1 :	<pre>RESULT 8 US-09-925-065A-103590 ; Sequence 103590, Application US/09925065A publication No. US20040181048A1 GENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135 CURRENT FILING DATE: 2001-08-08 FRIOR APPLICATION NUMBER: US 60/243,096 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-10-24 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 SOFTWARE: FastSRD for Windows Version 4.0 SEQ ID NO 103590 LENGTH: 645</pre>
2006005/56441 N: Identifiction and Mapping of N: Identifiction and Mapping of N: In the Human Genome 08827.137 00827.137 2002-11-21 2001-03-10 NUMBER: US 10/215,598 2001-08-09 NUMBER: US 60/311,695 : 2001-08-10 NUMBER: US 60/311,695 : 2001-08-10 NOS: 1226818 for Windows Version 4.0 epien	vid G. Identification and Mapping Nucleotide Polymorphisms 827.135 WDMBER: US/09/925,065A 2001-08-08 UMBER: US 60/243,096 2000-11-20 UMBER: US 60/252,147 2000-11-20 UMBER: US 60/250,092 2000-11-30 UMBER: US 60/250,092 2001-11-30 UMBER: US 60/261,766 2001-01-16 2001-01-16 2001-01-16 2001-05-09 S: 957086 S: 957086 or Windows Version 4.0
N: in the Human Genome 08027.137 ON NUMBER: US/10/301,480 TB: 2002-11-21 NUMBER: US 10/215,598 : 2002-08-09 NUMBER: US 60/311,695 : 2001-08-10 NOG: 1226818 for Windows Version 4.0 Apien	<b></b>
TB: 2002-11-21 NUMBER: US 10/215,598 : 2002-08-09 NUMBER: US 60/311,695 : 2001-08-10 NOS: 1226618 for Windows Version 4.0 apien 201 2%. Score 12.6: DB 9:	PRIOR APELICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24 PRIOR FILING DATE: 2000-11-20 PRIOR FILING DATE: 2000-11-20 PRIOR APELICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-11-30 PRIOR APELICATION NUMBER: US 60/261,766 PRIOR APELICATION NUMBER: US 60/261,766 PRIOR APELICATION NUMBER: US 60/261,766 PRIOR APELICATION NUMBER: US 60/261,846 PRIOR APELICATION NUMBER: US 60/289,846 PRIOR APELICATION NUMBER: US 60/289,846 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 103590 LENGTH: 645
LING DATE: 2002-08-09 LICATION NUMBER: US 60/311,695 SIG ID NOS: 1226818 PastESEQ For Windows Version 4.0 203835 625 4: Homo sapien 4: Homo sapien 4: Homo Sapien 4: Homo Sapien 4: Homo Sapien 4: Homo Sapien	LING DATE: 2000-11-20 PLICATION NUMBER: US 6 PLICATION NUMBER: US 6 LING DATE: 2000-11-30 PLICATION NUMBER: US 6 LING DATE: 2001-01-16 PLICATION NUMBER: US 6 PLICATION PLICATION NUMBER: US 6 PLICATION PLICATION NUMBER: US 6 PLICATION PLICATION
NOS: 1226818 for Windows Version 4.0 apien 21 2%. Score 12.6: DB 9:	LING DAYE: 2000-11-30 LICATION WUMBER: US 6 LICATION WUMBER: US 6 LICATION WUMBER: US 6 LICATION WUMBER: US 6 SEQ ID NOS: 957086 FastSEQ for Windows 103590 645
apien 31 3% - Score 12 5, DB 9:	LILCATION NUMBER: US 0 LING DATE: 2001-05-09 7 SEQ ID NOS: 957086 FASESEQ for Windows 103590 645
21 28: Score 12.6: DB 9:	103590
.7;	TYPE: DNA
hes 56; Conservative 0; Mismatches 39; Indels 0; Gaps	/ UKGAWAISM: FOUND BAPTEND US-09-925-065A-103590
DY 57 TAAAATGGGGAAACATTGCAAGCAAGCAAACAACACACAC	Query Match 21.2%; Score 32.6; DB 6; Length 645; Best Local Similarity 58.9%; Pred. No. 1.8; Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
DY 117 CCTTGEAGCTGEGGCAGAGGTCAGAGACCTCTCTG 151	$\begin{array}{llllllllllllllllllllllllllllllllllll$
RESULT 7 JS-10-301-480-817244 ; Sequence 817244, Application US/10301480 ; Publication No. US20060057564A1	OY 117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151 
GENERAL INCOMPATION: G. G. G. TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms TITLE OF INVENTION: In the Human Genome FILE REFERCE: 108827.137 FILE REFERCE: 108827.137 CURRENT APPLICATION NUMBER: US/10/301,480	RESULT 9 US-10-301-480-203834 ; Sequence 203834, Application US/10301480 ; publication No. US20060057564A1 ; GENERAL INFORMATION: ; GENERAL INFORMATION:
; CURRENT FILING DATE: 2002-11-21 ; PRIOR APPLICATION NUMBER: US 10/215,598 ; PRIOR FILING DATE: 2002-08-09 ; PRIOR APPLICATION NUMBER: US 60/311,695	NVENTION: Identif NVENTION: in the ENCE. 108827.137
<pre>PRIOR FILING DATE: 2001-08-10 NUMBER OF SEQ ID NOS: 1226818 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 817244</pre>	CURRENT FILLAGE DATE: 2002-11-21 PRIOR APPLICATION NUMBER: US 10/215,598 PRIOR FILLING DATE: 2002-08-09 PRIOR FILLING DATE: 2002-08-09
; LENGIH: 642 ; TYPE: DNA ; ORGANISM: Homo sapien US-10-301-480-817244	FILING DATE: 2001-08-10 VOF SEQ ID NOS: 1226816 ARE: FastSEQ for Windows NG 203834
Query Match 21.2%; Score 32.6; DB 10; Length 625; Best Local Similarity 58.9%; Pred. No. 1.7; Matches 56; Conservative 0; Mismatches 39; Indels 0; Gaps 0;	ວິລີສິດ
OY 57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAAACAGCCCTGCCTG	Query Match 20.9%; Score 32.2; DB 9; Length 625; Best Local Similarity 57.9%; Pred. No. 2.4; Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;
QY       117       CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG       151         Db       105       GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG       139	$ \begin{array}{c} \texttt{Oy} \qquad \qquad \texttt{57}  TAAAATGGGCAAACATTGCAAGCAGCAGCAAACAGCACACACGCCTCCCTGCCTG$

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; Query Match 20.9%; Score 32.2; DB 6; Length 645;	<pre>PRIOR PILLING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR PILLING DATE: 2001-01-16 PRIOR PILLING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 957086 SOFTWARE: PastSEQ for Windows Version 4.0 SOFTWARE: PastSEQ for Windows Version 4.0 LENGTH: 645 TYPE: DNA CRGANISM: Homo sapiens US-09-925-065A-103589</pre>	NVENTION ENCE: 100 ENCE: 100 PLICATION LICATION ICATION 1 ICATION 1 ICATION 1	RESULT 11 US-09-925-065A-103589 ; Sequence 103589, Application US/09925065A ; Publication No. US20040181048A1 ; GENERAL INFORMATION: • ADDITIONT. WARD DAVID G	Qy       57 TAAAATGGGCAAACATTGCAAGCAGCAAACAGCAGAGCAGCAGCCCTCCCT	; ORGANISM: Homo sapien US-10-301-480-817243 Query Match 20.9%; Score 32.2; DB 10; Length 625; Best Local Similarity 57.9%; Pred. No. 2.4; Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0;	CURRENT APPLICATION NUMBER: US/10/301,480 CURRENT PILLING DATE: 2002-11-21 PRIOR APPLICATION NUMBER: US 10/215,598 PRIOR RILING DATE: 2002-08-09 PRIOR PILLING DATE: 2002-08-09 PRIOR PILLING DATE: 2002-08-10 NUMBER OP SEQ ID NOS: 1226818 SOPTWARE: PABLERQ For Windows Version 4.0 SEQ ID NO 817243 LENGTH: 625		DD 45 TGAAAAGGGGAGAAATTGATAGGAGATAAACTCAAAGACAGAGGCAGCAGTTCYTGCAGA 104 Oy 117 CCTTGGAGCTGGGGCAGAGGTCAGAGACCTCTCTG 151                       DD 105 GCCTTGTAGAGGTAAAGAGGTCATATTTTATTCTG 139
APPLICATION N			Query Match       20.6%;       Score 31.8, DB 6;       Length 662;         Best Local Similarity       51.8%;       Pred. No. 3.3;       Mismatches       67;       Indels       0;       Gaps       0;         Matches       72;       Conservative       0;       Mismatches       67;       Indels       0;       Gaps       0;         Qy       11       TGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAAATGGGCAAAAC       70       11 <t< td=""><td>B: FastSEQ for Windows Version 4.0 782496 : 662 DNA DNA SM: Homo sapiens SM: Homo sapiens</td><td>יפדיפדיפה</td><td><pre>FUDICATION NO. US2004014104941 GENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135 CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT APPLICATION NUMBER: US 60/243,096 FRIOR APPLICATION NUMBER: US 60/252,147 FRIOR FILING DATE: 2000-11-20 FRIOR FILING DATE: 2000-11-20</pre></td><td>Qy       117 CCTTGGAGCTGGGGCAGAGGGTCAGAGACCTCTCTG       151         Db       125 GCCTTGTAGAGGTAAAGAGGTCATATTTATTCTG       159         RESULT 12       12       125-065A-782496/c         US-09-925-065A-782496/c       US/09925065A         ; Sequence 782496, Application US/09925065A</td><td>Best Local Similarity 57.9%; Pred. No. 2.4; Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0; Cy 57 TAAAATGGGCAAACATTGCAAGCAAGCAAGAGAAAACACCACAGCCCTGCCTG</td></t<>	B: FastSEQ for Windows Version 4.0 782496 : 662 DNA DNA SM: Homo sapiens SM: Homo sapiens	יפדיפדיפה	<pre>FUDICATION NO. US2004014104941 GENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135 CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT APPLICATION NUMBER: US 60/243,096 FRIOR APPLICATION NUMBER: US 60/252,147 FRIOR FILING DATE: 2000-11-20 FRIOR FILING DATE: 2000-11-20</pre>	Qy       117 CCTTGGAGCTGGGGCAGAGGGTCAGAGACCTCTCTG       151         Db       125 GCCTTGTAGAGGTAAAGAGGTCATATTTATTCTG       159         RESULT 12       12       125-065A-782496/c         US-09-925-065A-782496/c       US/09925065A         ; Sequence 782496, Application US/09925065A	Best Local Similarity 57.9%; Pred. No. 2.4; Matches 55; Conservative 1; Mismatches 39; Indels 0; Gaps 0; Cy 57 TAAAATGGGCAAACATTGCAAGCAAGCAAGAGAAAACACCACAGCCCTGCCTG

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RESULT 14 US-09-925-065A-370446/c ; Sequence 370446, Application US/09925065A ; Publication No. US20040181048A1 ; Publication No. RESULT 15 US-09-955-065A-370447/c ; Sequence 370447, Application US/09925065A ; Publication No. US20040181048A1 ; GENERAL INFORMATION: ; APPLICANT: Wang, David G. ; TITLE OF INVENTION: Identification and Mapping of Single Ş 昂 Ś 昂 Ś 昂 Ś 昂 US-11-124-367A-5038 SEQ ID NO 5038 LENGTH: 24675 Matcheg Query Match SEQ ID NO 370446 Matches Best Local Similarity Query Match TYPE: DNA ORGANISM: Homo sapiens -09-925-065A-370446 Best Local PRIOR FILING DATE: 2004-06-25 PRIOR APPLICATION NUMBER: US 60/599,554 PRIOR FILING DATE: 2004-08-09 PRIOR CURRENT FILING DATE: 2001-06-08 PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20 SOFTWARE: FastSEQ for Windows Version 4.0 NUMBER OF SEQ ID NOS: APPLICANT: Wang, David G. TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135 SOFTWARE: FastSEQ for Windows Version 4.0 NUMBER OF SEQ ID NOS: CURRENT APPLICATION NUMBER: US/09/925,065A TYPE: DNA ORGANISM: Homo sapiens ENGTH: 18237 18177 APPLICATION NUMBER: US 60/289,846 FILING DATE: 2001-05-09 APPLICATION NUMBER: US 60/250,092 FILING DATE: 2000-11-30 APPLICATION NUMBER: US 60/261,766 FILING DATE: 2001-01-16 197 61; 64 GGCANACATTGCAAGCAGCAAACAGCAAACACACACCCCT 103 62 TGGGCANACATTGCAAGCAGCAAACAGCAAACACACACCCCTCCCTGCCT 111 57; 611 2 TTTGTGTGCCGCCCCCGAAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAAA 61 \$ Similarity AGTACTTACGTTGCAATCAGCAAGATGCACAAACACTCCTCCCCACCCT 18286 TTTGCAGACTGCCTCCCCTAGCCGGGAGGTCTGTTTTTCCCGGCTACTGGTGACAAGTATA 18236 TGTGTGCCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATG 63 TTTTTGCAATCACACATTGCCAGACTATGCTAAGTTCAGCATAGTCATTCTCCAAAAGTG 138 Conservative Conservative 20.5%; 34460 20.3%; 957086 Score 31.2; DB 6; Pred. No. 5; 0; Mismatches 43; 0; Mismatches Score 31.6; Pred. No. 13; DB 14; 49; 43; Length 611; Length 24675; Indels Indels <u>,</u> <u>,</u> Gaps Gaps <u>,</u> 0

뭥 Search completed: April 18, 2006, 15:39:40 Job time : 95.5846 secs 昂 Ş Ś ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-925-065A-370447 Query Match Best Local Similarity Matches 57; Conservat SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 370447 NUMBER OF SEQ ID NOS: 957086 PRIOR PRIOR APPLICATION NUMBER: US 60/261,766 PRIOR FILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/252,147 PRIOR FILING DATE: 2000-11-20 PRIOR APPLICATION NUMBER: US 60/250,092 PRIOR FILING DATE: 2000-11-30 PRIOR APPLICATION NUMBER: US 60/243,096 PRIOR FILING DATE: 2000-10-24 CURRENT APPLICATION NUMBER: US/09/925,065A CURRENT FILING DATE: 2001-08-08 FILB TITLE OF INVENTION: Nucleotide Polymorphisms PRIOR FILING DATE: ENGTH: **REFERENCE:** APPLICATION NUMBER: US 60/289,846 197 137 64 GGCAAACATTGCAAGCAGCAAACAGCAAACACACAGCCCT 103 4 611 TTTTTGCAATCACACATTGCCAGACTATGCTAAGTTCAGCATAGTCATTCT IGIGIGCTCCTCTGAAGTCCCACACTGAACAAACTTCAGCCTACTCAIGTCCCTAAAAAIG 63 GACACACACACACACACACACACACATACACACAT 98 Conservative 108827.135 2001-05-09 20.3%; 0; Mismatches Score 31.2; Pred. No. 5; DB 6; ĥ 43; the Human Genome Length 611; Indels 0 CCAAAAGTG 138 Gaps

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19.7         11558         6         PCT-US93-06251-23         Sequence         23, App           19.6         80706         3         US-09-949-016-15347         Sequence         15347           19.6         80706         3         US-09-669-751-144         Sequence         17009           19.1         205163         3         US-09-949-016-17009         Sequence         17009,           19.0         606         3         US-09-949-016-17009         Sequence         1897,           19.0         2680         3         US-09-949-016-17240         Sequence         17240,           19.0         86213         3         US-09-949-016-17241         Sequence         17240,           19.0         86213         3         US-09-949-016-17241         Sequence         17240,           19.0         86213         3         US-09-949-016-17242         Sequence         17241,           19.0         86213         3         US-09-949-016-17242         Sequence         17242,           19.0         86213         3         US-09-949-016-17242         Sequence         17242,           18.7         748         748         3         US-09-949-016-172592         Sequence         27242,	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	print ion	atents NA: * afents NA: * ofptodata/1/ina ofptodata/1/ina ofptodata/1/ina ofptodata/1/ina ofptodata/1/ina ofptodata/1/ina ofptodata/1/ina ofptodata/1/ina	Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.         OM nucleic - nucleic search, using sw model         Run on:       April 18, 2006, 12:23:43 ; Search time 32.8522 Seconds (without alignments) B332.600 Million cell updates/sec         Title:       US-09-884-901A-8 Perfect score:         154       19ttgtgtgctgctctgaaggtcagagacctctctgggc 154         Scoring table:       IDENTITY NUC Gapop 10.0, Gapext 1.0         Searched:       1303057 seqs, 888780828 residues         Total number of hits satisfying chosen parameters:       2606114
Query Match       100.0%;       Score 154;       DB 3;       Length 774;         Best Local Similarity 100.0%;       Pred. No. 1.2e-40;       Indels 0;       Gaps 0;         Qy       1       GTTTGTGTGCGCGCCTCTGAAGTCCAACAGAAAAACTTCAGCCTACTCATGTCCCTAAA 60       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	144, 10 10	ABLE FORM: ABLE FORM: BALE FORM: BALE FORM: Ploppy IBM PC com PatentIn R PatentIn R PatentIn R	NO. 62 NO. 62 NL INFO LICANT L	-767-1	25       28.8       18.7       1762       2       US-06-105-483-300       Sequence 300, App         26       28.8       18.7       1762       2       US-08-709-209-300       Sequence 300, App         27       28.8       18.7       1762       2       US-08-709-209-300       Sequence 300, App         27       28.8       18.7       1762       2       US-09-949-016-12805       Sequence 300, App         28       28       18.7       126237       3       US-09-949-016-16674       Sequence 14093, A         29       28.8       18.7       126237       3       US-09-949-016-16675       Sequence 14093, A         20       28       18.4       126237       3       US-09-949-016-16675       Sequence 14093, A         20       34       18.4       126237       3       US-09-949-016-12805       Sequence 14093, A         20       34       18.4       19256       3       US-09-949-016-12805       Sequence 14093, A         20       34       18.4       19256       3       US-09-949-016-14060       Sequence 14805, A         20       3       28.2       18.3       3068       2       US-09-949-016-14392       Sequence 3.0, Appli

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RESULT 3 US-09-001-039B-65 ; Sequence 65, Application US/09001039B ; Patent No. 6818439 ; GENERAL INFORMATION: ; APPLICANT: Jolly, Douglas J.	Gy       1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 60         Db       9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 68         Gy       61 AFGGGCAAACATTGCAAGCAGC 82	Query Match 53.2%; Score 82; DB 3; Length 90; Best Local Similarity 100.0%; Pred. No. 2.2e-17; Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ATTORNEY/AGENT LINFORMATION: NAME: MCMASEers, David D. REGISTRATION UMBER: 33,963 REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4 TELEFONGULATION INFORMATION: TELEFHONE: (206) 682-6031 INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHANACTERISTICS: LENGTH: 90 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOCY: linear MOLECULE TYPE: DNA (genomic) US-09-001-039B-61	186 <sup>-1</sup> \$2558	APPLICANT: Greengard, JUGITH APPLICANT: Greengard, JUGITH TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF TITLE OF INVENTION: OF HEMOPHILIA AND OTHER DISORDERS NUMBER OF SEQUENCES: 04 CORRESPONDENCE ADDRESS: ADDRESSE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 CITY: Seattle STATE: Washington COUNTRY: U.S.A.	Qy         121 GGAGCTGGGGCAGAGGTCAGAGACCTCTCTGGGC 154
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昂 8 昂 8 US-09-001-039B-67/c **RESULT 4** US-09-001-039B-65 ; Sequence 67, ; Patent No. 68 ; GENERAL INFC Query Match Best Local S Matches 82 TELEPAX: (206) 682-6031 INFORMATION FOR SEC ID NO: 65 SEQUENCE CHARACTERISTICS: LENGTH: 90 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/99/001,039B FLLING DATE: 13-UAN-1998 CLASSIFICATION INFORMATION: NAME: MCMASTERS, David D. REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 APPLICANT: Jolly, I APPLICANT: Chang, : APPLICANT: Respess APPLICANT: DePolo, APPLICANT: Ibanez, C APPLICANT: Greengard APPLICANT: Lee, Will TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: APPLICANT : APPLICANT : TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER APPLICANT: APPLICANT : CORRESPONDENCE ADDRESS: ADDRESSEB: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300 APPLICANT : APPLICANT : NUMBER OF SEQUENCES: APPLICANT: APPLICANT: STREET: 701 Fifth CITY: Seattle STATE: Washington ZIP: 98104 COUNTRY : INFORMATION: OF SEQUENCES : 82; 9 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAACTTCAGCCTACTCATC 7, Application US/09001039B 6818439 1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA Similarity Jolly, Douglas J. Chang, Stephen M.W. Respess, James G. DePolo, Nicholas J. Hsu, David Chi-Tang Ibanez, Carlos E. Greengard, Judith Lee, Will Chang, Stephen M.W. Respess, James G. DePolo, Nicholas J. Hsu, David Chi-Tang Ibanez, Carlos B. Conservative U.S.A. Greengard, Judith Lee, Will DNA (genomic) METHODS FOR ADMINISTRATION OF RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT OF HEMOPHILIA AND OTHER DISORDERS 53.2%; Score 82; DB 100.0%; Pred. No. 2.2 Live 0; Mismatches METHODS FOR ADMINISTRATION OF RECOMBINANTGENE DELIVERY VEHICLES OF HEMOPHILIA AND OTHER DISORDERS 84 84 65: DB 3; Le 2.2e-17; <u>.</u> Length 90 Indels FOR TREATMENT <u>,</u> CCCTANA 68 Gaps 60 0

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Ş US-09-001-039B-63/c RESULT 5 昂 昂 Ş US-09-001-039B-67 Sequence 63, Matches Query Match Best Local Similarity GENERAL TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: ( tent No. APPLICANT: APPLICANT: NAME: McMasters, David D. REGISSTRATION NUMBER: 33,963 REPERSING/DOCKET NUMBER: 1155.005 / 930049.441C4 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 02 base pairs MOLECULE TYPE: COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: APPLICANT: APPLICANT: ATTORNEY / AGENT INFORMATION : CORRESPONDENCE ADDRESS : APPLICANT APPLICANT: APPLICANT: APPLICANT: APPLICATION NUMBER: FILING DATE: 13-JAL CLASSIFICATION: CITY: Seattle STATE: Washington COUNTRY: U.S.A. TOPOLOGY : STRANDEDNESS: TYPE: STATE : STREET : ZIP: 98104 STREET : ZIP: COUNTRY : CITY: ADDRESSBE : COMPUTER: IBM PC compatible . OPERATING SYSTEM: PC-DOS/MS-DOS ADDRESSEE : 135 GETCAGAGACCTCTCTGG 152 INFORMATION: 22 82 78; 98104 Seattle 6818439 nucleic acid GGTCAGAGACCTCTCGG 5 Washington INVENTION: INVENTION: Application US/09001039B B: Seed Intellectual Property Law Group 701 Pifth Avenue, Suite 6300 701 Fifth Avenue, Suite Lee, Chang, Stephen M.W. Respess, James G. DePolo, Nicholas J. Greengard, Judith Hsu, David Chi-Tang Conservative Ibanez, Carlos E. Jolly, Douglas J. linear Seed Intellectual Property Law Group 1 Pifth Avenue, Suite 6300 DNA (genomic) 13-JAN-1998 single Will METHODS FOR ADMINISTRATION OF RECOMBINANTGENE DELIVERY VEHICLES OF HEMOPHILIA AND OTHER DISORDERS 50.6%; Score 78; DB 3; 100.0%; Pred. No. 4.4e-1 tive 0; Mismatches 84 US/09/001,039B 67: 4.4e-16; <u>,</u> Length 82; Indels FOR TREATMENT <u></u> Gaps 0 뭥 ; MOLECULE TYPE: DNA (genomic) US-09-001-039B-63 昂 ą Ś US-09-001-039B-64/c **RESULT 6** COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/001,039B FLLING DATE: 13-JAN-1998 CLASSIFICATION: ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 33,963 REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4 TELECOMMUNICATION INFORMATION: Matches Sequence 64, Application US/09001039B Patent No. 6818439 Query Match Best Local Similarity Matches 77; Conserv GENERAL INFORMATION: TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: APPLICANT : APPLICANT : SEQUENCE CHARACTERISTICS: REGISTRATION NUMBER: 33,963 REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4 TELECOMMUNICATION INFORMATION: SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: CORRESPONDENCE ADDRESS: TITLE OF INVENTION: APPLICANT : APPLICANT: APPLICANT APPLICANT: APPLICANT APPLICANT: FILING DATE: APPLICATION NUMBER: STREET: 701 Fi CITY: Seattle TOPOLOGY: linear STRANDEDNESS : TYPE: CLASSIFICATION: STATE : ZIP: 98104 COUNTRY: TELEPHONE : TELEPHONE : ADDRESSEE : LENGTH: NAMB: 135 GGTCAGAGACCTCTCTG 151 82 CAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGA 22 H: 82 base pairs nucleic acid DEDNESS: single McMasters, David GGTCAGAGACCTCTCTG 6 Washington B: Seed Intellectual Property Law Group 701 Fifth Avenue, Suite 6300 (206) 682-677 U.S.A. Jolly, Douglas J. Chang, Stephen M.W. Hsu, David Chi-Tang Ibanez, Carlos B. Respess, James G. DePolo, Nicholas J. Conservative Greengard, Judith Lee, Will (206) 622-4900 13-JAN-1998 METHODS FOR ADMINISTRATION OF RECOMBINANTGENE DELIVERY VEHICLES OF HEMOPHILIA AND OTHER DISORDERS 50.0%; Score 77; 100.0%; Pred. No. Live 0; Mismatcl 84 US/09/001,039B 63 : e. Mismatches 9.4e-16; DB 3; 0 ; Length 82; Indels FOR TREATMENT °. Gaps 22 0

RESULT 7 US-09-001-039B-68/c 昂 ą 昂 Ś **JS-09-001-039B-68** US-09-001-039B-64 Sequence 6t Patent No. Query Match Best Local S Query Match Matches TELEPHONE: (206) 622-49 TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: APPLICANT: Lee, Will TITLE OF INVENTION: 1 TITLE OF INVENTION: 1 TITLE OF INVENTION: 0 NUMBER OF SEQUENCES: GENERAL INFORMATION: TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 64: STRANDEDNESS: TOPOLOGY: lin MOLECULE TYPE: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM FC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/001,039B TELEPHONE: (206) 622-4900 SEQUENCE CHARACTERISTICS: ATTORNEY/AGENT INFORMATION: NAME: McMasters, David D. REGISTRATION NUMBER: 33,963 CORRESPONDENCE ADDRESS: APPLICANT: APPLICANT: APPLICANT: APPLICANT: MOLECULE TYPE: DNA (genomic) SEQUENCE CHARACTERISTICS: APPLICANT: APPLICANT: APPLICANT: ZIP: CLASSIFICATION: FILING DATE: COUNTRY: TYPE: STATE: CITY: STREET : ADDRESSEE : STRANDEDNESS: si TOPOLOGY: linear LENGTH: 78 base pairs TYPE: nucleic acid -ENGTH : 68, 14 61 ATGGGCAAACATTG 74 74 GTTTGTGTGCGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 15 74; н 98104 1: 78 base pairs nucleic acid Seattle 8, Application US/09001039B 6818439 Similarity Washington ATGGGCANACATTG 1 9 Jolly, Douglas J. Chang, Stephen M.W. Respess, James G. DePolo, Nicholas J. Heu, David Chi-Tang 701 Fifth Avenue, Suite U.S.A. Greengard, Judith Jolly, 48.1%; Score 74; ilarity 100.0%; Pred. No. Conservative 0; Mismatci linear Ibanez, Carlos E. TGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAA 60 Seed Intellectual Property Law Group )1 Fifth Avenue, Suite 6300 13-JAN-1998 DNA (genomic) single Will single METHODS FOR ADMINISTRATION OF RECOMBINANTGENE DELIVERY VEHICLES OF HEMOPHILIA AND OTHER DISORDERS 48.18; 84 68: Score 74; 1155.005 / 930049.441C4 Mismatches DB 3; Lo 8.8e-15; DB 3; <u>,</u> Length 78; Length 78; Indels FOR TREATMENT <u>,</u> Gaps 0 망 8 昂 Ş 片 Ş 망 Ş US-09-001-039B-66 US-09-001-039B-66 **RESULT 8** Matches Best Local Similarity Best Query Match Sequence 66, Patent No. Matches TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: GENERAL INFORMATION: REFERENCE/DOCKET NUMBER: 33,963 REFERENCE/DOCKET NUMBER: 115 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 TELEPAN' (200) COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/001,039B FILING DATE: 13-JAN-1998 CLASSIFICATION: TOPOLOGY: 11 MOLECULE TYPE: ATTORNEY/AGENT INFORMATION: NAME: McMasters, David D. REGISTRATION NUMBER: 33,5 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: TITLE OF INVENTION: TITLE OF INVENTION: APPLICANT: TITLE OF INVENTION: APPLICANT APPLICANT : APPLICANT: APPLICANT : APPLICANT: APPLICANT: APPLICANT: Local TYPE: nucleic acid STRANDEDNESS: single STREET: 701 Fi CITY: Seattle STATE: Washing COUNTRY: U.S.A. ZIP: ENGTH: ADDRESSEE : 143 ACCTCTCTGG 19 83 AAACAGCAAAACACAGAGCCCTCCCTGCCTGCCTGCTGGAGCTGGGGGCAGAGGGTCAGAG 142 74 н 14 5 70; 98104 1 GITTIGIGIGCTGCCTCTGAAGTCCACACIGAACAAACTTCAGCCTACTCATGTCCCCTAAA 60 74; Similarity 6818439 ACCTCTCTGG AAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGGCAGAGGTCAGAG ATGGGCAAACATTG 74 ATGGGCAAACATTG 1 GTTTGTGTGCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCCTAAA 15 Washington Application US/09001039B Ibanez, Carlos E. Greengard, Judith Lee, Will B: Seed Intellectual Property Law Group 701 Fifth Avenue, Suite 6300 70 base pairs 45.5%; Score 70; ilarity 100.0%; Pred. No. Conservative 0; Mismatc Jolly, Douglas J. Chang, Stephen M.W. Conservative linear Нвu, Respess, James G. DePolo, Nicholas J. DNA (genomic) David Chi-Tang 152 70 100.0%; F. METHODS FOR ADMINISTRATION OF RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT OF HEMOPHILIA AND OTHER DISORDERS 84 66: 1155.005 / 930049.441C4 Pred. No. 8.8e-15;
; Mismatches 0; Mismatches 1.7e-13; hes 0; DB 3; Length 70 Indels Indels 0; <u></u> Gaps Сарв 60 <u>,</u> 0

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RESULT 10 US-09-799-451-433/c 昂 Ş 昂 ş US-09-001-039B-62 RESULT US-09-001-039B-62 Matches Patent No. 6818439 GENERAL INFORMATION: Sequence 62, Sequence 4: Patent No. Query Match Best . SENERAL INFORMATION: APPLICANT: APPLICANT: APPLICANT: Tang, Y. Tom APPLICANT: Zhou, Ping TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: ( TITLE OF TITLE OF SOPTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/001,039B COMPUTER READABLE FORM: MEDIUM TYPE: Floppy MOLECULE TYPE: SEQUENCE CHARACTERISTICS: TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900 ATTORNEY/AGENT INFORMATION: CORRESPONDENCE ADDRESS : NUMBER OF SEQUENCES: APPLICANT : APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: TITLE OF APPLICANT : **NPPLICANT:** LICANT CITY: Seattle STATE: Washington STREET : TOPOLOGY : STRANDEDNESS : NAME: McMasters, David D. REGISTRATION NUMBER: 33,963 REFERENCE/DOCKET NUMBER: 11 PILING DATE: 1 CLASSIFICATION: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS ADDRESSEE : COUNTRY : Local Similarity ENGTH: 143 ACCTCTCTG 151 433, Application US/09799451 p. 6783969 83 AAACAGCAAACACACAGCCCTCCCTGCCTGCTGACCTTGGAGCTGGGGCAGAGGTCAGAG 142 61 щ ; 69 H: 70 base pairs nucleic acid 98104 AAACAGCAAACACAGCCCTCCCTGCCTGCTGACCTTGCAGCTGGGGCAGAGGTCAGAG INVENTION: INVENTION: INVENTION: Goodrich, Ryle Asundi, Vinod Ren, Feiyan Accretere Application US/09001039B B: Seed Intellectual Property Law Group 701 Fifth Avenue, Suite 6300 Chang, Stephen M.W. Respess, James G. DePolo, Nicholas J. U.S.A. Greengard, Judith Conservative Lee, Hsu, David Chi-Tang Jolly, Douglas J. banez, Carlos E. linea 13-JAN-1998 DNA (genomic) single Will 69 METHODS FOR ADMINISTRATION OF RECOMBINANTGENE DELIVERY VEHICLES FOR TREATMENT OF HEMOPHILIA AND OTHER DISORDERS 44.8%; Score 69; DB 3; Length 70; 100.0%; Pred. No. 3.7e-13; 84 62: 1155.005 / 930049.441C4 °. Mismatches °. Indels 0 Gaps 60 0 昂 ₽ Ş Ş Ś NAMB/KEY: CDS LOCATION: (1)..(1746) US-09-799-451-433 ; ORGANISM: Human US-09-949-016-17561 US-09-949-016-17561 RESULT 11 NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for SEQ ID NO 17561 NUMBER OF SEQ ID NOS: 948 SOPTWARE: pt\_FL\_genes Version 2.0 SEQ ID NO 433 SEQ ID NO 433 Query Match Best Local Similarity Matches Query Match Best Local Similarity GENERAL INFORMATION: Sequence 17561, A Patent No. 681233 Matches CURRENT APPLICATION NUMBER: US/09/799,451 CURRENT FILING DATE: 2001-03-05 APPLICANT : APPLICANT : APPLICANT : APPLICANT : PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 FILE REFERENCE: 803 APPLICANT: Drmanac, Radoje T. MITLE OF INVENTION: No. 6783969el Nucleic Acids MITLE OF INVENTION: Polypeptides TYPE: DNA ORGANISM: Homo sapiens FEATURE: PPLICANT TYPE: DNA PPLICANT: PPLICANT: PPLICANT : PPLICANT PPLICANT : PPLICANT PPLICANT LENGTH: 2018 LENGTH : 1857 93 CACACAGCCCTCCCTGCCT 111 49; 58; 113379 FastSEQ for Windows Version 4.0 CACCCAGCCCCCCTGGCCT 1839 Zhang, Jie Xue, Aidong J. Zhao, Qing A. Wang, Dunrui Yang, Yonghong Wehrman, Tom Wehrman, Tom Ghosh, Reena Yamazaki, Victo Chen, Rui-hong Wang, wang Conservative Conservative Application US/09949016 Yunqing Jian-Rui Zhiwej Victoria 20.1%; 207012 20.1%; 62.0%; 0; Mismatches 0; Mismatches Score 31; DB Pred. No. 15;

APPLICANT: VENTER, J. Craig et al. APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOOI307 FILE REFERENCE: CLOOI307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-03 1917 CACAGITGCGCTCATTCATGTCTCGAATAGCGGCATGCT 33 САЛАСТІСАСССТАСТСАТСТССТАЛАЛОСССАЛАСАТІССАЛССАССАЛАСАССАЛА 92 
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Ś **RESULT 13** 8 昂 Ş PCT-US93-06251-23/c ; ORGANISM: Human US-09-949-016-17562 Ş US-09-949-016-17562 **RESULT 12** 昂 B GENERAL INFORMATION: Sequence 17562, Application US/09949016 patent No. 6812339 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CL001307 SOFTWARE: Fast SEQ ID NO 17562 Matches Best Query Match PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 PRIOR PRIOR NUMBER OF SEQ ID NOS: 207012 PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 TYPE: DNA APPLICANT: Wickstrom, Eric and Rife, Jason P. TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphona NUMBER OF SEQUENCES: 93 LENGTH: 113379 ATTORNBY/AGENT INFORMATION: NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,346 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS APPLICATION NUMBER: P FILING DATE: 19930630 MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, STATE : CLASSIFICATION : COUNTRY : STREET : Local Similarity REFERENCE/DOCKET NUMBER: 8586 ZIP: ADDRESSEE : 67373 AGGCAAGCAACATAATGGAACTAGTCAAAAGTACCTAAGTGCT 67415 67313 GCCTTTGAAAACCCTTCCTGAATAGTTGTCAGACAATTGATTTTGAATAAAAATGGCACAAT 67372 67373 67313 GCCTTTGAAAACCCTTCCTGAATAGTTGTCAGACAATTGATTTTGAATAAAATGGCACAAT 67372 APPLICATION NUMBER: 60/241,755 FILING DATE: 2000-10-20 12 GCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAACA 71 72 58; 11530 Garden City NY FastSEQ for Windows Version 4.0 AGGCAAGCAACATAATGGAACTAGTCAAAAGTACCTAAGTGCT 67415 Application PC/TUS9306251 E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza USA Conservative 20.1%; 56.3%; PCT/US93/06251 , , Score 31; DB Pred. No. 15; Mismatches Version DB 3; Length 113379; #1.25 45; Indels ASSOCIATED OF DETECTION AND USES THEREOF Arylphosphonates 0; Gaps 0; Ş ; ORGANISM: Human ; PEATURE; ; NAME/KBY: misc\_feature ; LOCATION: (1):..(80706) ; OTHER INFORMATION: n = A,T,C or US-09-949-016-15347 **RESULT 15** 昂 昂 Ş 昂 昂 ą 昂 Ś Ş US-09-949-016-15347 **RESULT 14** PCT-US93-06251-23 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS SOFTWARE: FastSEO for Windows Version 4.0 SEQ ID NO 15347 LENGTH: 80706 Matches Sequence 15347, Application US/09949016 Patent No. 6812339 Query Match Best Local Similarity Matches Query Match Reac NUMBER OF SEQ ID NOS: 207012 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 PRIOR APPLICATION NUMBER: 60/237,768 TELEFAX: 516-742-4366 TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: PRIOR FILING DATE: 2000-10-03 FILE REFERENCE: CL001307 TYPE: DNA MOLECULE TYPE: DNA (genomic) TELECOMMUNICATION INFORMATION: LENGTH: 11558 base pairs TYPE: nucleic acid STRANDEDNESS: double Local STRANDEDNESS: do TOPOLOGY: linear 35147 35087 8096 9728 GCCCCCTCCGAGCTCCGACTTGGGCCCTCTTCAGTTCCCACTGGACCCTGATTTGAGCTG 9669 9668 GCTCTGGAAATAGCTGAGAACCCAGACGCGGGACGCAGGGGGCAAGGGCTCAAGGAGGAGA 9609 107 TECCTECTEACCTTEGAGCTEGEGECAGAGETCAGAGACCTCTCTEGE 153 129 47 59; 69 ACATIGCAAGCAGCAAACAGCAAACACACAGCCCTCCCTGCCTGACCTTGGAGCTGG 9 GCTGCCTCTGAAGTCCACACTGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGGCAA 68 70; h 19.7%; Similarity 51.5%; 70; Conservative CTCATGTCCCTAAAATGGGCAAACATTGCAAGCAAGCAAACAGCAAACACACAGCCCTCCC 106 AGCTGGCAGCAGGAGGAGCCGGGGGATGTGTGCTGTTATCTCTCTGCG 35193 GTCAGAGTCAAGAGGC 9593 GGCAGAGGTCAGAGAC 144 Conservative 516-742-4343 19.6%; 23: 0 Score 30.4; DE Pred. No. 10; 0; Mismatches 0 Score 30.2; Pred. No. 24; G Mismatches DB 3; DB 6; Length 11558; 48; 66; ASSOCIATED OF DETECTION AND USES THEREOF Length 80706; Indels Indels ... <u>,</u> Gaps Gaps 128 0 0,

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FaceLL NO. 000000 FaceLL NO. 000000 FaceLL NO. 000000 FaceLL CANT: Greenspan, Ralph J. FITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Methods for Identifying Compounds for TITLE OF INVENTION: Methods for Identifying Compounds for FILE REFERENCE: P-NI 3864 CURRENT FILL OF INVENTION: Balance and the Perception of Gravity FILE REFERENCE: P-NI 3864 CURRENT FILLING DATE: 2000-09-26 PRIOR APPLICATION NUMBER: US/09/669,751 CURRENT FILLING DATE: 2000-09-26 PRIOR FILLING DATE: 2000-09-26 PRIOR FILLING DATE: 2000-09-26 VINMBER OF SEQ ID NOS: 260 NUMBER: US 60/168,579 FRIOR FILLING DATE: 1999-12-02 NUMBER OF SEQ ID NOS: 261 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 144 LENGTH: 658 FTER: DNA CORGANISM: Drosophila US-09-669-751-144 Search completed: April 18, 2006, 12:30:28 Job time : 34.8522 secs 昂 Ş 昂 Ş US-09-669-751-144/c ; Sequence 144, Application US/09669751 ; Patent No. 6551575 Query Match 19.5%; Score 30; DB 3; Length 658; Best Local Similarity 53.4%; Pred. No. 5; Matches 63; Conservative 0; Mismatches 55; Indels 392 Cricarricrigicarcagarricrigicarcagarricrigicarcaratricrigicarcagarricgicaaa 333 10 CTGCCTCTGAAGTCCACACATGAACAAACTTCAGCCTACTCATGTCCCTAAAATGGGCAAA 69 0; Gaps 0